GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 13:28:23 ; Search time 1452.41 Seconds
(without alignments)
10479.665 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	523	100.0	523	6	AX147746	AX147746 Sequence
2	523	100.0	523	6	AX300783	AX300783 Sequence
3	467.4	89.4	517	6	AX147742	AX147742 Sequence
4	467.4	89.4	517	6	AX300779	AX300779 Sequence
5	409	78.2	471	6	AX147754	AX147754 Sequence
6	409	78.2	471	6	AX300791	AX300791 Sequence
7	364.8	69.8	1536	10	BC012409	BC012409 Mus muscu
8	361.6	69.1	798	10	RNIGFI2	X06108 Rat mRNA (c
9	361.6	69.1	958	10	RNIGFI1	X06107 Rat mRNA (c
10	358.4	68.5	710	10	RATIGFIA	M15480 Rat insulin
11	356.8	68.2	539	6	AX147744	AX147744 Sequence
12	356.8	68.2	539	6	AX300781	AX300781 Sequence
13	349.4	66.8	651	10	MMIGFIBR	X04482 Mouse mRNA
14	336	64.2	432	4	AF022961	AF022961 Oryctolag
15	334.4	63.9	7260	6	AX375028	AX375028 Sequence
16	334.4	63.9	7260	6	AX411095	AX411095 Sequence
17	334.4	63.9	7260	9	HSIGFACI	X57025 Human IGF-I
18	332.8	63.6	666	6	A29119	A29119 H.sapiens I
19	332.8	63.6	725	9	HSIGFI	X00173 Homo sapien
20	332.8	63.6	728	9	HUMGFII	M29644 Human insul
21	332.4	63.6	616	9	HSIGF1A	X56773 H.sapiens m
22	331.2	63.3	620	6	I08370	I08370 Sequence 2
23	331.2	63.3	1076	9	HUMIGFI	M27544 Human insul
24	316.8	60.6	444	9	HSU40870	U40870 Human alter
25	293.8	56.2	532	4	SSILGF1M	X17492 Porcine mRN
26	293.8	56.2	567	4	PIGGFIIA	M31175 Pig insulin
27	286.2	54.7	888	4	ECU85272	U85272 Equus cabal
28	281.8	53.9	978	4	GOTIGFI	D11378 Goat mRNA f
29	281.8	53.9	978	6	E05279	E05279 DNA encodin
30	280.2	53.6	1284	4	BTILGF1A	X15726 Bovine mRNA
31	275.4	52.7	747	4	SHPIGFIA6	M31735 Sheep insul
32	275.4	52.7	790	4	SHPIGFIA21	M31734 Sheep insul
33	275.4	52.7	1015	4	SHPIGFIA46	M31736 Sheep insul
34	275.4	52.7	1107	4	SHPIGFIA1	M30653 Sheep insul
35	275.2	52.6	730	9	HSIGF1B	X56774 H.sapiens m
36	275.2	52.6	1094	9	HUMGFIB	M11568 Human insul
37	275.2	52.6	1136	6	E01349	E01349 cDNA encodi
38	275.2	52.6	1136	6	I08009	I08009 Sequence 3
39	273.6	52.3	612	9	HUMIGFIB	M37484 Human insul
40	271.6	51.9	696	10	MMIGFIAR	X04480 Mouse mRNA
41	268.4	51.3	513	10	RATGJIL	M17714 Rat insulin
42	268.4	51.3	521	10	RNIGFIR	X06043 Rat mRNA fo
43	268.4	51.3	836	10	CPIGF1	X52951 Guinea pig
44	266.8	51.0	1052	10	RATIGF1A	D00698 Rattus sp.
45	263.6	50.4	1346	10	RATIGFIB	M15481 Rat insulin

ALIGNMENTS

RESULT 1
AX147746
LOCUS AX147746 523 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 5 from Patent WO0136483.
ACCESSION AX147746
VERSION AX147746.1 GI:14346791
KEYWORDS .
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 523)
AUTHORS Goldspink,G.R. and Johnson,I.R.
TITLE Use of the insulin-like-growth factor i isoform mgf for the
treatment of neurological disorders

```
  JOURNAL   Patent: WO 0136483-A 5 25-MAY-2001;
            University College London (GB)
FEATURES             Location/Qualifiers
     source          1. .523
                     /organism="Oryctolagus cuniculus"
                     /db_xref="taxon:9986"
     CDS             <1. .336
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC41177.1"
                     /db_xref="GI:14346792"
                     /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
                     DECCFRSCDLRRLEMYCAPLKPAKAARSVRAQRHTDMPKTQKYQPPSTNKKMKSQRRR
                     KGSTFEEHK"
BASE COUNT      154 a    129 c    142 g     98 t
ORIGIN

  Query Match           100.0%;  Score 523;  DB 6;  Length 523;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-150;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523


RESULT 2
AX300783
LOCUS       AX300783                523 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 5 from Patent WO0185781.
ACCESSION   AX300783
VERSION     AX300783.1  GI:17382064
KEYWORDS    .
SOURCE      rabbit.
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1
  AUTHORS   Goldspink,G.D. and Terenghi,G.B.
  TITLE     Repair of nerve damage
  JOURNAL   Patent: WO 0185781-A 5 15-NOV-2001;
            University College London (GB) ; East Grinstead Medical Research
            Trust (GB)
FEATURES             Location/Qualifiers
     source          1. .523
                     /organism="Oryctolagus cuniculus"
                     /db_xref="taxon:9986"
     CDS             <1. .336
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD13042.1"
                     /db_xref="GI:17382065"
                     /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
                     DECCFRSCDLRRLEMYCAPLKPAKAARSVRAQRHTDMPKTQKYQPPSTNKKMKSQRRR
                     KGSTFEEHK"
BASE COUNT      154 a    129 c    142 g     98 t
ORIGIN

  Query Match           100.0%;  Score 523;  DB 6;  Length 523;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-150;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523


RESULT 3
AX147742
LOCUS       AX147742                517 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 1 from Patent WO0136483.
ACCESSION   AX147742
VERSION     AX147742.1  GI:14346787
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 517)
  AUTHORS   Goldspink,G.R. and Johnson,I.R.
  TITLE     Use of the insulin-like-growth factor i isoform mgf for the
            treatment of neurological disorders
```

```
  JOURNAL   Patent: WO 0136483-A 1 25-MAY-2001;
            University College London (GB)
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             <1. .333
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC41175.1"
                     /db_xref="GI:14346788"
                     /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
                     DECCFRSCDLRRLEMYCAPLKPAKSARSVRAQRHTDMPKTQKYQPPSTNKNTKSQRRK
                     GSTFEEHK"
BASE COUNT      150 a    130 c    139 g     98 t
ORIGIN

  Query Match             89.4%;  Score 467.4;  DB 6;  Length 517;
  Best Local Similarity   96.2%;  Pred. No. 3.4e-133;
  Matches  501;  Conservative    0;  Mismatches   16;  Indels    4;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||||||||||||| |||||||||||||||||| | ||||||||   |
Db        241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 521
              |||||||||||||||||||||||||||||||||||||||||
Db        477 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 517


RESULT 4
AX300779
LOCUS       AX300779                517 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 1 from Patent WO0185781.
ACCESSION   AX300779
VERSION     AX300779.1  GI:17382060
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Goldspink,G.D. and Terenghi,G.B.
  TITLE     Repair of nerve damage
  JOURNAL   Patent: WO 0185781-A 1 15-NOV-2001;
            University College London (GB) ; East Grinstead Medical Research
            Trust (GB)
FEATURES             Location/Qualifiers
     source          1. .517
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             <1. .333
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD13040.1"
                     /db_xref="GI:17382061"
                     /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
                     DECCFRSCDLRRLEMYCAPLKPAKSARSVRAQRHTDMPKTQKYQPPSTNKNTKSQRRK
                     GSTFEEHK"
BASE COUNT      150 a    130 c    139 g     98 t
ORIGIN

  Query Match             89.4%;  Score 467.4;  DB 6;  Length 517;
  Best Local Similarity   96.2%;  Pred. No. 3.4e-133;
  Matches  501;  Conservative    0;  Mismatches   16;  Indels    4;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||||||||||||| |||||||||||||||||| | ||||||||   |
Db        241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 521
              |||||||||||||||||||||||||||||||||||||||||
Db        477 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 517


RESULT 5 .
AX147754
LOCUS       AX147754                471 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 13 from Patent WO0136483.
ACCESSION   AX147754
VERSION     AX147754.1  GI:14348552
KEYWORDS    .
SOURCE      rabbit.
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1  (bases 1 to 471)
  AUTHORS   Goldspink,G.R. and Johnson,I.R.
  TITLE     Use of the insulin-like-growth factor i isoform mgf for the
            treatment of neurological disorders
```

```
  JOURNAL   Patent: WO 0136483-A 13 25-MAY-2001;
            University College London (GB)
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="Oryctolagus cuniculus"
                     /db_xref="taxon:9986"
     CDS             <1. .318
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC41264.1"
                     /db_xref="GI:14348553"
                     /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
                     DECCFRSCDLRRLEMYCAPLKPAKAARSVRAQRHTDMPKTQKEVHLKNTSRGSAGNKN
                     YRM"
BASE COUNT      132 a    118 c    131 g     90 t
ORIGIN

  Query Match           78.2%;  Score 409;  DB 6;  Length 471;
  Best Local Similarity   90.1%;  Pred. No. 3.8e-115;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||
Db        241 ATGCCCAAGACTCAG---------------------------------------------- 255

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471


RESULT 6
AX300791
LOCUS       AX300791                471 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 13 from Patent WO0185781.
ACCESSION   AX300791
VERSION     AX300791.1  GI:17382072
KEYWORDS    .
SOURCE      rabbit.
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1
  AUTHORS   Goldspink,G.D. and Terenghi,G.B.
  TITLE     Repair of nerve damage
  JOURNAL   Patent: WO 0185781-A 13 15-NOV-2001;
            University College London (GB) ; East Grinstead Medical Research
            Trust (GB)
FEATURES             Location/Qualifiers
     source          1. .471
                     /organism="Oryctolagus cuniculus"
                     /db_xref="taxon:9986"
     CDS             <1. .318
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD13045.1"
                     /db_xref="GI:17382073"
                     /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
                     DECCFRSCDLRRLEMYCAPLKPAKAARSVRAQRHTDMPKTQKEVHLKNTSRGSAGNKN
                     YRM"
BASE COUNT      132 a    118 c    131 g     90 t
ORIGIN

  Query Match           78.2%;  Score 409;  DB 6;  Length 471;
  Best Local Similarity   90.1%;  Pred. No. 3.8e-115;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||
Db        241 ATGCCCAAGACTCAG---------------------------------------------- 255

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471


RESULT 7
BC012409
LOCUS       BC012409                1536 bp    mRNA    linear   ROD 07-AUG-2002
DEFINITION  Mus musculus, Similar to insulin-like growth factor 1, clone
            MGC:18617 IMAGE:4194295, mRNA, complete cds.
ACCESSION   BC012409
VERSION     BC012409.1  GI:15214568
KEYWORDS    MGC.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1536)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
```

```
  JOURNAL   Submitted (15-AUG-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Baylor College of Medicine Human Genome
            Sequencing Center
            Center code: BCM-HGSC
            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
            Contact: amg@bcm.tmc.edu
            Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
            Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
            Richards, S., Gibbs, R.A.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 24 Row: k Column: 11
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 6754307.
FEATURES             Location/Qualifiers
     source          1. .1536
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /map="FVB/N"
                     /clone="MGC:18617 IMAGE:4194295"
                     /tissue_type="Liver, normal. 5 month old male mouse."
                     /clone_lib="NCI_CGAP_Li9"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             28. .429
                     /codon_start=1
                     /product="Similar to insulin-like growth factor 1"
                     /protein_id="AAH12409.1"
                     /db_xref="GI:15214569"
                     /translation="MSSSHLFYLALCLLTFTSSTTAGPETLCGAELVDALQFVCGPRG
                     FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPTKAARSIRAQRHTD
                     MPKTQKSPSLSTNKKTKLQRRRKGSTFEEHK"
BASE COUNT      485 a    324 c    303 g    424 t
ORIGIN

  Query Match             69.8%;  Score 364.8;  DB 10;  Length 1536;
  Best Local Similarity   83.2%;  Pred. No. 2.1e-101;
  Matches  441;  Conservative    0;  Mismatches   82;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||||
Db         94 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 153

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||||| || |||||||||| ||||||||||||||||
Db        154 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 213

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||||| ||||||||||||||||||||||||||| ||||||||||||
Db        214 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 273

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  |||| ||||||||||  ||||||||||||||||||| |||
Db        274 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 333

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        334 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 393

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||| |||
Db        394 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 453

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| |   |||| | || | ||  ||||||||| ||||||
Db        454 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 513

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||          |  |||||| | || |||  |||       || |||||||   ||
Db        514 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 573

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              ||||| ||||||| ||||||||||||||||||||| ||||||||||||
Db        574 ACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATTC 623


RESULT 8
RNIGFI2
LOCUS       RNIGFI2                 798 bp    mRNA    linear   ROD 12-SEP-1993
DEFINITION  Rat mRNA (clone IGF1AB2) for insulin-like growth factor I.
ACCESSION   X06108 M32339 Y00429
VERSION     X06108.1  GI:56426
KEYWORDS    insulin-like growth factor I.
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 798)
  AUTHORS   Rotwein,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1987) Rotwein P., Washington University, School
            of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO
            63110, USA
REFERENCE   2  (bases 1 to 798)
  AUTHORS   Shimatsu,A. and Rotwein,P.
  TITLE     Sequence of Two Rat Insulin-like Growth Factor I mRNAs Differing
            Within the 5' Untranslated Region
  JOURNAL   Nucleic Acids Res. 15 (1987) In press
COMMENT     Another IGF-I mRNA of rat liver differing in the 5' UT-region is
            described in <X06107>.
FEATURES             Location/Qualifiers
     source          1. .798
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="liver"
     misc_feature    1. .72
                     /note="5' UT-region"
     CDS             73. .552
                     /note="IGF-I (AA 1-159)"
                     /codon_start=1
                     /protein_id="CAA29481.1"
                     /db_xref="GI:56427"
                     /translation="MGKISSLPTQLFKICLCDFLKIKIHIMSSSHLFYLALCLLTFTS
                     SATAGPETLCGAELVDALQFVCGPRGFYFNKPTGYGSSIRRAPQTGIVDECCFRSCDL
                     RRLEMYCAPLKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRRKGSTLEEHK"
     misc_feature    553. .798
                     /note="3' UT-region"
BASE COUNT      238 a    196 c    183 g    181 t
ORIGIN

  Query Match             69.1%;  Score 361.6;  DB 10;  Length 798;
  Best Local Similarity   82.8%;  Pred. No. 1.9e-100;
  Matches  439;  Conservative    0;  Mismatches   84;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| |||||||||||||| ||||||||||||||||||||||
Db        217 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 276

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| |||||||||||||||||| || |||||||||| ||||||||||| |||
Db        277 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 336

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||||| |||||||||||||||||||||||||||||||||||||||
```

```
Db        337 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 396

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  ||||| |||| || ||| |||| ||||||||||||||| |||
Db        397 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 456

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  ||||| | ||| ||  |||||||| ||||   || |||
Db        457 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 516

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| ||||||||||||||||||| ||||||||||||||| |||
Db        517 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 576

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db        577 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 636

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||          |  |||||| |||| ||| ||||      || ||| ||||  ||
Db        637 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 696

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        697 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 746


RESULT 9
RNIGFI1
LOCUS       RNIGFI1                   958 bp    mRNA    linear   ROD 12-SEP-1993
DEFINITION  Rat mRNA (clone IGF1AB1) for insulin-like growth factor I.
ACCESSION   X06107 M32260 Y00429
VERSION     X06107.1  GI:56424
KEYWORDS    insulin-like growth factor I.
SOURCE      Rattus norvegicus.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 958)
  AUTHORS   Rotwein,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-OCT-1987) Rotwein P., Washington University, School
            of Medicine, 660 South Euclid Avenue, Box 8127, St. Louis, MO
            63110, USA
REFERENCE   2  (bases 1 to 958)
  AUTHORS   Shimatsu,A. and Rotwein,P.
  TITLE     Sequence of two rat insulin-like growth factor I mRNAs differing
            within the 5' untranslated region
  JOURNAL   Nucleic Acids Res. 15 (17), 7196 (1987)
  MEDLINE   88015572
   PUBMED   3658684
COMMENT     Another IGF-I mRNA of rat liver differing in the 5' UT-region is
            described in <X06108>.
FEATURES             Location/Qualifiers
     source          1. .958
                     /organism="Rattus norvegicus"
                     /strain="Srpague-Dawley"
                     /db_xref="taxon:10116"
                     /tissue_type="liver"
     misc_feature    1. .258
                     /note="5' UT-region"
     CDS             259. .738
                     /note="IGF-I (AA 1-159)"
                     /codon_start=1
                     /protein_id="CAA29480.1"
                     /db_xref="GI:56425"
                     /db_xref="SWISS-PROT:P08024"
                     /translation="MGKISSLPTQLFKICLCDFLKIKIHIMSSSHLFYLALCLLTFTS
                     SATAGPETLCGAELVDALQFVCGPRGFYFNKPTGYGSSIRRAPQTGIVDECCFRSCDL
                     RRLEMYCAPLKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRRKGSTLEEHK"
     misc_feature    736. .958
                     /note="3' UT-region"

BASE COUNT      260 a    246 c    209 g    243 t
ORIGIN

  Query Match           69.1%;  Score 361.6;  DB 10;  Length 958;
  Best Local Similarity   82.8%;  Pred. No. 1.9e-100;
  Matches  439;  Conservative    0;  Mismatches   84;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| |||||||||||||| ||||||||||||||||||||||
Db        403 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 462

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| |||||||||||||||| || |||||||||| |||||||||||| |||
Db        463 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 522

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        523 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 582

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  ||||| |||| || ||| |||| ||||||||||||||| |||
Db        583 TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 642

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  ||||| | ||| ||  |||||||| ||||   || |||
Db        643 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 702

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| ||||||||||||||||||| ||||||||||||||| |||
Db        703 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 762

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db        763 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 822

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||          |  |||||| |||| ||| ||||      || ||| ||||  ||
Db        823 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 882

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        883 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 932


RESULT 10
RATIGFIA
LOCUS       RATIGFIA                  710 bp    mRNA    linear   ROD 27-APR-1993
DEFINITION  Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.
ACCESSION   M15480
VERSION     M15480.1  GI:204749
KEYWORDS    growth factor; insulin-like growth factor.
SOURCE      Rat (Sprague-Dawley) adult liver cDNA to mRNA, clone pRIGF-1-42.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 710)
  AUTHORS   Roberts,C.T. Jr., Lasky,S.R., Lowe,W.L. Jr., Seaman,W.T. and
            LeRoith,D.
  TITLE     Molecular cloning of rat insulin-like growth factor I complementary
            deoxyribonucleic acids: differential messenger ribonucleic acid
            processing and regulation by growth hormone in extrahepatic tissues
  JOURNAL   Mol. Endocrinol. 1 (3), 243-248 (1987)
  MEDLINE   88288198
   PUBMED   3453891
COMMENT     Draft entry and computer-readable copy of sequence in [Mol.
            Endocrinol. (1987) In press] kindly
            provided by S.R.Lasky, 16-MAR-1987.
FEATURES             Location/Qualifiers
     source          1. .710
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     CDS             106. .507
```

```
                     /note="insulin-like growth factor precursor"
                     /codon_start=1
                     /protein_id="AAA41385.1"
                     /db_xref="GI:204750"
                     /translation="MSSSHLFYLALCLLTFTSSATAGPETLCGAELVDALQFVCGPRG
                     FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTD
                     MPKTQKSQPLSTHKKRKLQRRRKGSTLEEHK"
     sig_peptide     106. .171
                     /note="insulin-like growth factor signal peptide"
     mat_peptide     172. .258
                     /product="insulin-like growth factor B peptide"
     mat_peptide     259. .294
                     /product="insulin-like growth factor C peptide"
     mat_peptide     295. .357
                     /product="insulin-like growth factor A peptide"
     mat_peptide     358. .381
                     /product="insulin-like growth factor D peptide"
     mat_peptide     382. .504
                     /product="insulin-like growth factor E peptide"
BASE COUNT      202 a    191 c    172 g    145 t
ORIGIN      1 bp upstream of EcoRI site.

  Query Match             68.5%;  Score 358.4;  DB 10;  Length 710;
  Best Local Similarity   82.5%;  Pred. No. 1.8e-99;
  Matches  437;  Conservative    0;  Mismatches   86;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||| ||||||||||||||||||||||||
Db        172 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 231

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| |||||||||||||||||| || |||||||||| |||||||||||| |||
Db        232 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAG 291

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        292 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 351

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||  | |  ||||||  ||||| |||| || ||| |||| ||||||||||||||| |||
Db        352 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 411

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  ||||| | ||| ||  |||||||| ||||   || |||
Db        412 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 471

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| ||||||||||||||||||| |||||||||||||||| |||
Db        472 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 531

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db        532 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 591

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| |||| ||| ||||      || ||| ||||  ||
Db        592 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 651

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
               ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        652 CCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 701


RESULT 11
AX147744
LOCUS       AX147744                539 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 3 from Patent WO0136483.
ACCESSION   AX147744
VERSION     AX147744.1  GI:14346789
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 539)
  AUTHORS   Goldspink,G.R. and Johnson,I.R.
  TITLE     Use of the insulin-like-growth factor i isoform mgf for the
            treatment of neurological disorders
  JOURNAL   Patent: WO 0136483-A 3 25-MAY-2001;
            University College London (GB)
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
     CDS             <1. .336
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC41176.1"
                     /db_xref="GI:14346790"
                     /translation="GPETLCGAELVDALQFVCGPRGFYFNKPTVYGSSIRRAPQTGIV
                     DECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRR
                     KGSTLEEHK"
BASE COUNT      161 a    136 c    139 g    103 t
ORIGIN

  Query Match             68.2%;  Score 356.8;  DB 6;  Length 539;
  Best Local Similarity   82.3%;  Pred. No. 5.4e-99;
  Matches  436;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||| ||||||||||||||||||||||||
Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| |||||||||||||||||   || |||||||||| |||||||||||| |||
Db         61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||  | |  ||||||  ||||| |||| || ||| |||| ||||||||||||||| |||
Db        181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  ||||| | ||| ||  |||||||| ||||   || |||
Db        241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| ||||||||||||||||||| |||||||||||||||| |||
Db        301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db        361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    |||||| |||| ||| ||||      || ||| ||||  ||
Db        421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
               ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530


RESULT 12
AX300781
LOCUS       AX300781                539 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 3 from Patent WO0185781.
ACCESSION   AX300781
VERSION     AX300781.1  GI:17382062
KEYWORDS    .
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
```

```
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
           Rattus.
REFERENCE  1
  AUTHORS  Goldspink,G.D. and Terenghi,G.B.
  TITLE    Repair of nerve damage
  JOURNAL  Patent: WO 0185781-A 3 15-NOV-2001;
           University College London (GB) ; East Grinstead Medical Research
           Trust (GB)
FEATURES             Location/Qualifiers
     source          1. .539
                     /organism="Rattus sp."
                     /db_xref="taxon:10118"
     CDS             <1. .336
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD13041.1"
                     /db_xref="GI:17382063"
                     /translation="GPETLCGAELVDALQFVCGPRGFYFNKPTVYGSSIRRAPQTGIV
                     DECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTDMPKTQKSQPLSTHKKRKLQRRR
                     KGSTLEEHK"
BASE COUNT      161 a    136 c    139 g    103 t
ORIGIN

  Query Match           68.2%;  Score 356.8;  DB 6;  Length 539;
  Best Local Similarity  82.3%;  Pred. No. 5.4e-99;
  Matches  436;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||| ||||||||||||||||||||
Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| ||||||||||||||||  || ||||||||| |||||||||| |||
Db         61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              |||| | | |||||| ||||| |||| || ||| |||| ||||||||||||| |||
Db        181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||| ||||| | ||| || ||||||||| |||| || |||
Db        241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| |||||||||||||||||| |||||||||||||| |||
Db        301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||    | || | || | ||||||| || ||||||
Db        361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |   |||||| |||| ||| ||||      || ||| ||||  ||
Db        421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
               ||||||| |||| |||||||||| |||||||||||||||||||||||
Db        481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530


RESULT 13
MMIGFIBR
LOCUS       MMIGFIBR                651 bp    mRNA    linear   ROD 21-MAR-1995
DEFINITION  Mouse mRNA for preproinsulin-like growth factor IB.
ACCESSION   X04482
VERSION     X04482.1  GI:51805
KEYWORDS    growth factor; insulin-like growth factor IB; preproinsulin-like
            growth factor IB; signal peptide.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 651)
  AUTHORS   Bell,G.I., Stempien,M.M., Fong,N.M. and Rall,L.B.
  TITLE     Sequences of liver cDNAs encoding two different mouse insulin-like
            growth factor I precursors
  JOURNAL   Nucleic Acids Res. 14 (20), 7873-7882 (1986)
  MEDLINE   87040760
   PUBMED   3774549
COMMENT     The sequence is identical to the preproIGF-IA sequence (X04480)
            except for the presence of a 52 bp insertion following codon 86
            (position 397 to 448), caused by alternative RNA splicing. The B
            domain of IGF comprises residues 1-29 (position 139-225), the C
            domain residues 30-41 (position 226-261), the A domain residues
            42-62 (position 262-324) and the D domain residues 63-70 (position
            325-348).
FEATURES             Location/Qualifiers
     source          1. .651
                     /organism="Mus musculus"
                     /strain="Balb/c"
                     /db_xref="taxon:10090"
                     /clone="migfl-4"
                     /tissue_type="liver"
     misc_feature    43. .45
                     /note="pot. translation start"
     CDS             73. .474
                     /note="prepro IGF-IB (aa -22 to 111)"
                     /codon_start=1
                     /protein_id="CAA28170.1"
                     /db_xref="GI:51807"
                     /db_xref="MGD:MGI:96432"
                     /db_xref="SWISS-PROT:P05018"
                     /translation="MSSSHLFYLALCLLTFTSSTTAGPETLCGAELVDALQFVCGPRG
                     FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPTKAARSIRAQRHTD
                     MPKTQKSPSLSTNKKTKLQRRRKGSTFEEHK"
     sig_peptide     73. .138
     mat_peptide     139. .348
                     /product="mature IGF-IB (aa 1-70)"
     misc_feature    349. .471
                     /note="COOH-terminal peptide (E domain) (aa 71 to 111)"
     polyA_site      651_
                     /note="polyA site"
BASE COUNT      193 a    185 c    149 g    124 t
ORIGIN

  Query Match           66.8%;  Score 349.4;  DB 10;  Length 651;
  Best Local Similarity  82.8%;  Pred. No. 1.1e-96;
  Matches  425;  Conservative    0;  Mismatches   81;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||
Db        139 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 198

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| |||||||||||||||| || ||||||||| |||||||||||||||||
Db        199 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 258

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| ||||||||||||||||||||||||||| ||||||||||
Db        259 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || ||||| |||| |||||||||| ||||||||||||||||| |||
Db        319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 378

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||| | | | ||| || |||||||||| |||| || |||
Db        379 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||
```

```
Db        439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| |   ||||   | || | ||   |||||||||| ||||||
Db        499 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 558

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |    ||||||  | || |||  |||      || |||||||   ||
Db        559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAA 506
              ||||| |||||| ||||||||||||||||||
Db        619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651


RESULT 14
AF022961
LOCUS       AF022961                 432 bp    mRNA    linear   MAM 14-OCT-1997
DEFINITION  Oryctolagus cuniculus insulin-like growth factor IB (IGF-IB) mRNA,
            complete cds.
ACCESSION   AF022961
VERSION     AF022961.1  GI:2522201
KEYWORDS    .
SOURCE      Oryctolagus cuniculus.
  ORGANISM  Oryctolagus cuniculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1  (bases 1 to 432)
  AUTHORS   Flekna,G., Brem,G. and Mueller,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-SEP-1997) Institute of Animal Breeding and Genetics,
            Veterinary University of Vienna, Veterinaerplatz 1, Vienna A-1210,
            Austria
FEATURES             Location/Qualifiers
     source          1. .432
                     /organism="Oryctolagus cuniculus"
                     /strain="ZIKA hybrid strain"
                     /db_xref="taxon:9986"
                     /cell_type="primary liver cells"
                     /tissue_type="liver"
     gene            1. .432
                     /gene="IGF-IB"
     CDS             1. .432
                     /gene="IGF-IB"
                     /codon_start=1
                     /product="insulin-like growth factor IB"
                     /protein_id="AAB80950.1"
                     /db_xref="GI:2522202"
                     /translation="MITPTVKMRILSSSHLFYLALCLLTFTSSATAGPETLCGAELVD
                     ALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPAKAA
                     RSVRAQRHTDMPKTQKYQPPSTNKKMKSQRRRKGSTFEEHK"
BASE COUNT      105 a    126 c    115 g     86 t
ORIGIN

  Query Match           64.2%;  Score 336;  DB 4;  Length 432;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-92;
  Matches  336;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 156

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 216

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 276

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 336

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 396

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAG 336
              ||||||||||||||||||||||||||||||||||||
Db        397 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAG 432


RESULT 15
AX375028
LOCUS       AX375028                 7260 bp    DNA     linear   PAT 01-MAR-2002
DEFINITION  Sequence 31 from Patent WO0210436.
ACCESSION   AX375028
VERSION     AX375028.1  GI:19169860
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Baak,J. and Mutter,G.L.
  TITLE     Prognostic classification of breast cancer
  JOURNAL   Patent: WO 0210436-A 31 07-FEB-2002;
            THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; Baak, Jan (US)
FEATURES             Location/Qualifiers
     source          1. .7260
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT     2330 a   1415 c   1240 g   2275 t
ORIGIN

  Query Match           63.9%;  Score 334.4;  DB 6;  Length 7260;
  Best Local Similarity  84.6%;  Pred. No. 6.7e-92;
  Matches  445;  Conservative    0;  Mismatches   26;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                      |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||  ||||||||||||  |||| ||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACAT 478
              |||||||| |||||||| ||||| |||||| ||| ||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
```

Search completed: June 15, 2003, 17:22:10
Job time : 1454.41 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 09:07:57 ; Search time 158.655 Seconds
(without alignments)
7423.602 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	523	100.0	523	22	AAD06400	Rabbit IGF-I isofo
2	523	100.0	523	24	AAS16879	Rabbit mechano-gro
3	523	100.0	553	18	AAT84893	Rabbit insulin lik
4	467.4	89.4	517	22	AAD06398	Human IGF-I isofor
5	467.4	89.4	517	24	AAS16877	Human mechano-grow
6	409	78.2	471	22	AAD06405	Rabbit liver-type
7	409	78.2	471	24	AAS16884	Rabbit insulin-lik
8	356.8	68.2	539	22	AAD06399	Rat IGF-I isoform
9	356.8	68.2	539	24	AAS16878	Rat mechano-growth
10	334.4	63.9	818	8	AAN70436	Sequence encoding
11	334.4	63.9	7260	24	ABK84583	Human cDNA differe
12	334.4	63.9	7260	24	ABN97244	Gene #3742 used to
13	334.4	63.9	7260	24	ABK64812	Human benign prost
14	334.4	63.9	7260	24	ABK35504	Human endometrial
15	334.4	63.9	7260	24	ABK35561	Gene IGF1 differen
16	332.8	63.6	777	18	AAT84894	Human insulin like
17	331.2	63.3	622	7	AAN60490	Human prepro-somat
18	281.8	53.9	978	14	AAQ47804	Sequence encoding
19	275.2	52.6	1136	8	AAN70435	Sequence encoding
20	274.6	52.5	3599	19	AAV50428	Plasmid pIG0552 lo
21	274.6	52.5	3599	19	AAV40796	Actual sequence of
22	274.6	52.5	3600	19	AAV50427	Plasmid pIG0552 up
23	274.6	52.5	3600	19	AAV40795	Expected sequence
24	274.6	52.5	5707	20	AAX88055	Plasmid pIG0335 DN
25	274.6	52.5	6345	20	AAX88054	Plasmid pIG0100A D
26	273.6	52.3	612	22	AAS14695	Human cDNA encodin
27	266.8	51.0	1052	20	AAX27498	Rat liver form of
28	262	50.1	487	22	AAD06404	Rat liver-type IGF
29	262	50.1	487	24	AAS16883	Rat insulin-like g
30	237.6	45.4	317	24	AAS16882	Human insulin-like
31	237.6	45.4	318	22	AAD06403	Human liver-type I
32	237.6	45.4	462	19	AAV50426	Human IGF-1 encodi
33	237.6	45.4	462	19	AAV40794	Human IGF-I coding
34	237.6	45.4	462	24	ABL91699	Human polynucleoti
35	193	36.9	210	24	ABA03146	Native mature IGF-
36	191.4	36.6	237	12	AAQ13568	Beta-gal/IGF-1 fus
37	191.4	36.6	238	12	AAQ13569	Beta-gal/IGF-1 fus
38	191.4	36.6	2862	19	AAV26283	Recombinant botuli
39	187	35.8	4532	24	AAD32015	Bovine alpha lacta
40	186.6	35.7	210	24	AAD32016	Human insulin-like
41	185.2	35.4	240	13	AAQ23303	Synthetic human IG
42	185.2	35.4	390	18	AAT63526	Killer toxin leade
43	183.4	35.1	462	19	AAV50425	Human IGF-1 encodi
44	183.4	35.1	462	19	AAV40793	Optimised IGF-I co
45	180.2	34.5	207	22	AAH22139	Truncated human in

ALIGNMENTS

RESULT 1
AAD06400
ID AAD06400 standard; cDNA; 523 BP.
XX
AC AAD06400;
XX
DT 10-AUG-2001 (first entry)
XX
DE Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW sex-linked muscular dystrophy; peripheral neuropathy;
KW Alzheimer's disease; Parkinson's disease; ss.
XX
OS Oryctolagus cuniculus.
XX
FH Key Location/Qualifiers
FT CDS 1..336
FT /*tag= a
FT /product= "Mechano-growth factor (MGF)"
FT /note= "This region comprises exons 3-6. The CDS does
FT not include start codon"
FT /partial
XX
PN WO200136483-A1.
XX
PD 25-MAY-2001.
XX

```
PF   15-NOV-2000; 2000WO-GB04354.
XX
PR   15-NOV-1999;   99GB-0026968.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
XX
PI   Goldspink G,  Johnson I;
XX
DR   WPI; 2001-355620/37.
DR   P-PSDB; AAE02449.
XX
PT   Use of mechano-growth factor, an isoform of Insulin-like Growth
PT   Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT   medicament for the treatment of neurological disorder -
XX
PS   Claim 4; Page 53-54; 66pp; English.
XX
CC   The present invention relates to use of mechano-growth factor (MGF),
CC   an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC   medicament for the treatment of neurological disorder. The MGF is capable
CC   of reducing motoneurone loss by 20% or greater in response to nerve
CC   avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC   rescue. The MGF polynucleotide and polypeptide are useful in the
CC   manufacture of a medicament for the treatment of a neurological disorder,
CC   including a disorder of motoneurones and/or neurodegenerative disorder,
CC   e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC   spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC   poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC   toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC   injury that affects motoneurones, motoneurone loss associated with aging,
CC   autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC   peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC   The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
CC   isoform having extracellular (Ec) domain, hence also referred as
CC   IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC   nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC   of MGF.
XX
SQ   Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

  Query Match             100.0%;  Score 523;  DB 22;  Length 523;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-144;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523


RESULT 2
AAS16879
ID   AAS16879 standard; cDNA; 523 BP.
XX
AC   AAS16879;
XX
DT   25-FEB-2002  (first entry)
XX
DE   Rabbit mechano-growth factor (MGF) cDNA.
XX
KW   Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW   neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW   muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW   nerve avulsion.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..336
FT                   /*tag=  a
FT                   /product= "Rabbit MGF"
FT                   /partial
FT                   /note= "No start codon"
FT   exon            1..76
FT                   /*tag=  b
FT                   /number= 3
FT   exon            77..259
FT                   /*tag=  c
FT                   /number= 4
FT   exon            260..309
FT                   /*tag=  d
FT                   /number= 5
FT   exon            311..333
FT                   /*tag=  e
FT                   /number= 6
XX
PN   WO200185781-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-GB02054.
XX
PR   10-MAY-2000; 2000GB-0011278.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
PA   (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI   Goldspink G,  Terenghi G;
XX
DR   WPI; 2002-055585/07.
DR   P-PSDB; AAU10561.
XX
PT   Use of insulin-like growth factor I (IGF-I) isoform known as
PT   mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT   ability to reduce motoneuron loss in response to nerve avulsion, to
PT   treat nerve damage  -
XX
PS   Disclosure; Fig 7; 65pp; English.
XX
CC   The invention relates to the use of an insulin-like growth factor I
CC   (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC   of a medicament for treating nerve damage in the peripheral nervous
CC   system, or for treating nerve damage by localising MGF at the site of
CC   damage. The nerve damage may include severing of a nerve. The treatment
CC   may be combined with another treatment (such as a polypeptide growth
```

```
CC   factor other than MGF) that prevents or diminishes degeneration of the
CC   target organ (for example, muscle) which the damaged nerve innervates,
CC   whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC   MGF prevents or diminishes degeneration. The method is useful for
CC   treating neurological disorders, preferably motorneuron disorders. These
CC   methods can reduce motoneuron loss by 20% or greater in response to nerve
CC   avulsion. This sequence represents cDNA encoding the rabbit MGF.
XX
SQ   Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

  Query Match             100.0%;  Score 523;  DB 24;  Length 523;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-144;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523


RESULT 3
AAT84893
ID   AAT84893 standard; cDNA; 553 BP.
XX
AC   AAT84893;
XX
DT   14-APR-1998  (first entry)
XX
DE   Rabbit insulin like growth factor 1 encoding cDNA.
XX
KW   Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;
KW   heart; neuromuscular disease; primer; ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..366
FT                   /*tag=  a
FT                   /product= "IGF-1"
XX
PN   WO9733997-A1.
XX
PD   18-SEP-1997.
XX
PF   11-MAR-1997;   97WO-GB00658.
XX
PR   11-MAR-1996;   96GB-0005124.
XX
PA   (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI   Goldspink G;
XX
DR   WPI; 1997-470877/43.
DR   P-PSDB; AAW23301.
XX
PT   Use of insulin like growth factor I characterised by presence of Ec
PT   peptide - to treat humans or animals, particularly muscle disorders,
PT   heart conditions or neuromuscular diseases
XX
PS   Disclosure; Fig 3; 33pp; English.
XX
CC   A use of insulin like growth factor I (IGF-1) has been developed, and
CC   is characterised by the presence of the Ec peptide, or a functional
CC   equivalent, in the treatment or therapy of a human or animal. The IGF-1
CC   polypeptide can be used to treat muscular disorders, e.g. Duchenne or
CC   Becker muscular dystrophy, autosomal dystrophies and related progressive
CC   skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
CC   spinal cord injury induced muscle atrophy and neuromuscular diseases,
CC   and cardiac disorders, e.g. diseases where promotion of cardiac muscle
CC   protein synthesis is a beneficial treatment, cardiomyopathies and acute
CC   heart failure or insult, specifically myocarditis or myocardial
CC   infarction. It can also be used to promote bone fracture healing and
CC   maintenance of bone in old age. The present sequence encodes rabbit
CC   IGF-1 used in the present specification.
XX
SQ   Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;

  Query Match             100.0%;  Score 523;  DB 18;  Length 553;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-144;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
```

```
Db        511 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553


RESULT 4
AAD06398
ID   AAD06398 standard; cDNA; 517 BP.
XX
AC   AAD06398;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Human IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW   Human; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW   mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW   amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW   poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW   nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW   sex-linked muscular dystrophy; peripheral neuropathy;
KW   Alzheimer's disease; Parkinson's disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..333
FT                   /*tag=  a
FT                   /product= "Mechano-growth factor (MGF)"
FT                   /note= "This region comprises exons 3-6. The CDS does
FT                   not include start codon"
FT                   /partial
XX
PN   WO200136483-A1.
XX
PD   25-MAY-2001.
XX
PF   15-NOV-2000; 2000WO-GB04354.
XX
PR   15-NOV-1999;   99GB-0026968.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
XX
PI   Goldspink G,  Johnson I;
XX
DR   WPI; 2001-355620/37.
DR   P-PSDB; AAE02447.
XX
PT   Use of mechano-growth factor, an isoform of Insulin-like Growth
PT   Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT   medicament for the treatment of neurological disorder -
XX
PS   Claim 4; Page 49-50; 66pp; English.
XX
CC   The present invention relates to use of mechano-growth factor (MGF),
CC   an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC   medicament for the treatment of neurological disorder. The MGF is capable
CC   of reducing motoneurone loss by 20% or greater in response to nerve
CC   avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC   rescue. The MGF polynucleotide and polypeptide are useful in the
CC   manufacture of a medicament for the treatment of a neurological disorder,
CC   including a disorder of motoneurones and/or neurodegenerative disorder,
CC   e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC   spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC   poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC   toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC   injury that affects motoneurones, motoneurone loss associated with aging,
CC   autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC   peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC   The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
CC   isoform having extracellular (Ec) domain, hence also referred as
CC   IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC   nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC   of MGF.
XX
SQ   Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

  Query Match             89.4%;  Score 467.4;  DB 22;  Length 517;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-127;
  Matches  501;  Conservative    0;  Mismatches   16;  Indels    4;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || ||||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||| |||||||||||||| |||||||||||||||| | |||||||||   |
Db        241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 521
              |||||||||||||||||||||||||||||||||||||||||
Db        477 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 517


RESULT 5
AAS16877
ID   AAS16877 standard; cDNA; 517 BP.
XX
AC   AAS16877;
XX
DT   25-FEB-2002  (first entry)
XX
DE   Human mechano-growth factor (MGF) cDNA.
XX
KW   Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW   neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW   muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW   nerve avulsion.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..333
FT                   /*tag=  a
FT                   /product= "Human MGF"
FT                   /partial
FT                   /note= "No start codon"
FT   exon            1..76
FT                   /*tag=  b
FT                   /number= 3
FT   exon            77..259
FT                   /*tag=  c
FT                   /number= 4
FT   exon            260..307
```

```
FT                   /*tag=  d
FT                   /number= 5
FT   exon            308..330
FT                   /*tag=  e
FT                   /number= 6
XX
PN   WO200185781-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-GB02054.
XX
PR   10-MAY-2000; 2000GB-0011278.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
PA   (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI   Goldspink G,  Terenghi G;
XX
DR   WPI; 2002-055585/07.
DR   P-PSDB; AAU10559.
XX
PT   Use of insulin-like growth factor I (IGF-I) isoform known as
PT   mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT   ability to reduce motoneuron loss in response to nerve avulsion, to
PT   treat nerve damage  -
XX
PS   Claim 11; Fig 5; 65pp; English.
XX
CC   The invention relates to the use of an insulin-like growth factor I
CC   (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC   of a medicament for treating nerve damage in the peripheral nervous
CC   system, or for treating nerve damage by localising MGF at the site of
CC   damage. The nerve damage may include severing of a nerve. The treatment
CC   may be combined with another treatment (such as a polypeptide growth
CC   factor other than MGF) that prevents or diminishes degeneration of the
CC   target organ (for example, muscle) which the damaged nerve innervates,
CC   whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC   MGF prevents or diminishes degeneration. The method is useful for
CC   treating neurological disorders, preferably motorneuron disorders. These
CC   methods can reduce motoneuron loss by 20% or greater in response to nerve
CC   avulsion. This sequence represents cDNA encoding the human MGF.
XX
SQ   Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

  Query Match             89.4%;  Score 467.4;  DB 24;  Length 517;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-127;
  Matches  501;  Conservative    0;  Mismatches   16;  Indels    4;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||
Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||  |||||||||||||| |||||||||||||||| | |||||||||   |
Db        241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 521
              |||||||||||||||||||||||||||||||||||||||||
Db        477 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 517


RESULT 6
AAD06405
ID   AAD06405 standard; cDNA; 471 BP.
XX
AC   AAD06405;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
XX
KW   Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW   mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW   amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW   poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW   nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW   sex-linked muscular dystrophy; peripheral neuropathy;
KW   Alzheimer's disease; Parkinson's disease; liver; L.IGF-I; ss.
XX
OS   Oryctolagus cuniculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..318
FT                   /*tag=  a
FT                   /product= "Liver-type IGF-I isoform (L.IGF-I)"
FT                   /transl_except= (pos:7..9, aa:Gln)
FT                   /transl_except= (pos:25..27, aa:Gln)
FT                   /note= "These translation exceptions occur while decoding
FT                   the alternative version of the protein (AAE02456).
FT                   The CDS comprises exons 3, 4 and 6 and
FT                   does not include start codon"
FT                   /partial
XX
PN   WO200136483-A1.
XX
PD   25-MAY-2001.
XX
PF   15-NOV-2000; 2000WO-GB04354.
XX
PR   15-NOV-1999;   99GB-0026968.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
XX
PI   Goldspink G,  Johnson I;
XX
DR   WPI; 2001-355620/37.
DR   P-PSDB; AAE02452, AAE02456.
XX
PT   Use of mechano-growth factor, an isoform of Insulin-like Growth
PT   Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT   medicament for the treatment of neurological disorder -
XX
PS   Disclosure; Page 59-60; 66pp; English.
XX
CC   The present invention relates to use of mechano-growth factor (MGF),
CC   an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC   medicament for the treatment of neurological disorder. The MGF is capable
CC   of reducing motoneurone loss by 20% or greater in response to nerve
CC   avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC   rescue. The MGF polynucleotide and polypeptide are useful in the
CC   manufacture of a medicament for the treatment of a neurological disorder,
```

```
CC   including a disorder of motoneurones and/or neurodegenerative disorder,
CC   e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC   spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC   poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC   toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC   injury that affects motoneurones, motoneurone loss associated with aging,
CC   autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC   peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC   The present sequence is rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
CC   The L.IGF-I protein comprises amino acid sequences encoded by
CC   nucleic acid sequence of IGF-I exons 4 and 6.
XX
SQ   Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

  Query Match             78.2%;  Score 409;  DB 22;  Length 471;
  Best Local Similarity   90.1%;  Pred. No. 2.2e-110;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||
Db        241 ATGCCCAAGACTCAG---------------------------------------------- 255

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471


RESULT 7
AAS16884
ID   AAS16884 standard; cDNA; 471 BP.
XX
AC   AAS16884;
XX
DT   25-FEB-2002  (first entry)
XX
DE   Rabbit insulin-like growth factor I liver-type isoform (L.IGF-I) cDNA.
XX
KW   Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW   neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW   muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW   nerve avulsion; insulin-like growth factor I liver-type isoform; L.IGF-I;
XX
OS   Oryctolagus cuniculus.
XX
FH   Key             Location/Qualifiers

FT   CDS             1..318
FT                   /*tag= a
FT                   /product= "Rabbit L.IGF-I"
FT                   /partial
FT                   /note= "No start codon"
FT   exon            1..75
FT                   /*tag= b
FT                   /number= exon 3
FT   exon            76..258
FT                   /*tag= c
FT                   /number= exon 4
FT   exon            259..315
FT                   /*tag= d
FT                   /number= exon 6
XX
PN   WO200185781-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-GB02054.
XX
PR   10-MAY-2000; 2000GB-0011278.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
PA   (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI   Goldspink G,  Terenghi G;
XX
DR   WPI; 2002-055585/07.
DR   P-PSDB; AAU10564.
XX
PT   Use of insulin-like growth factor I (IGF-I) isoform known as
PT   mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT   ability to reduce motoneuron loss in response to nerve avulsion, to
PT   treat nerve damage  -
XX
PS   Disclosure; Fig 10; 65pp; English.
XX
CC   The invention relates to the use of an insulin-like growth factor I
CC   (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC   of a medicament for treating nerve damage in the peripheral nervous
CC   system, or for treating nerve damage by localising MGF at the site of
CC   damage. The nerve damage may include severing of a nerve. The treatment
CC   may be combined with another treatment (such as a polypeptide growth
CC   factor other than MGF) that prevents or diminishes degeneration of the
CC   target organ (for example, muscle) which the damaged nerve innervates,
CC   whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC   MGF prevents or diminishes degeneration. The method is useful for
CC   treating neurological disorders, preferably motorneuron disorders. These
CC   methods can reduce motoneuron loss by 20% or greater in response to nerve
CC   avulsion. This sequence represents cDNA encoding the rabbit insulin-like
CC   growth factor I liver-type isoform (L.IGF-I) used in experiments on
CC   motoneuron loss.
XX
SQ   Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

  Query Match             78.2%;  Score 409;  DB 24;  Length 471;
  Best Local Similarity   90.1%;  Pred. No. 2.2e-110;
  Matches  471;  Conservative    0;  Mismatches    0;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
```

```
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Db        241 ATGCCCAAGACTCAG---------------------------------------------- 255

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Db        256 -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Db        309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Db        369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523

Db        429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471
```

```
RESULT 8
AAD06399
ID   AAD06399 standard; cDNA; 539 BP.
XX
AC   AAD06399;
XX
DT   10-AUG-2001  (first entry)
XX
DE   Rat IGF-I isoform mechano-growth factor (MGF) cDNA.
XX
KW   Rat; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW   mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW   amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW   poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW   nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW   sex-linked muscular dystrophy; peripheral neuropathy;
KW   Alzheimer's disease; Parkinson's disease; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..336
FT                   /*tag= a
FT                   /product= "Mechano-growth factor (MGF)"
FT                   /note= "This region comprises exons 3-6. The CDS does
FT                   not include start codon"
FT                   /partial
XX
PN   WO200136483-A1.
XX
PD   25-MAY-2001.
XX
PF   15-NOV-2000; 2000WO-GB04354.
XX
PR   15-NOV-1999;   99GB-0026968.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
XX
PI   Goldspink G,  Johnson I;
XX
DR   WPI; 2001-355620/37.
DR   P-PSDB; AAE02448.
XX
PT   Use of mechano-growth factor, an isoform of Insulin-like Growth
PT   Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT   medicament for the treatment of neurological disorder -
XX
PS   Claim 4; Page 51-52; 66pp; English.
XX
CC   The present invention relates to use of mechano-growth factor (MGF),
CC   an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC   medicament for the treatment of neurological disorder. The MGF is capable
CC   of reducing motoneurone loss by 20% or greater in response to nerve
CC   avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC   rescue. The MGF polynucleotide and polypeptide are useful in the
CC   manufacture of a medicament for the treatment of a neurological disorder,
CC   including a disorder of motoneurones and/or neurodegenerative disorder,
CC   e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC   spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC   poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC   toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC   injury that affects motoneurones, motoneurone loss associated with aging,
CC   autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC   peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC   The present sequence is rat IGF-I isoform MGF cDNA. MGF is a muscle
CC   isoform having extracellular (Ec) domain, hence also referred as
CC   IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC   nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC   of MGF.
XX
SQ   Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;
```

```
  Query Match             68.2%;  Score 356.8;  DB 22;  Length 539;
  Best Local Similarity   82.3%;  Pred. No. 5.5e-95;
  Matches  436;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Db         61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Db        121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Db        181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Db        241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Db        301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Db        361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474

Db        421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523

Db        481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530
```

```
RESULT 9
AAS16878
ID   AAS16878 standard; cDNA; 539 BP.
XX
AC   AAS16878;
XX
DT   25-FEB-2002  (first entry)
XX
DE   Rat mechano-growth factor (MGF) cDNA.
```

```
XX
KW   Rat; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW   neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW   muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss;
KW   nerve avulsion.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..336
FT                   /*tag=  a
FT                   /product= "Rat MGF"
FT                   /partial
FT                   /note= "No start codon"
FT   exon            1..75
FT                   /*tag=  b
FT                   /number= exon 3
FT   exon            76..258
FT                   /*tag=  c
FT                   /number= exon 4
FT   exon            259..309
FT                   /*tag=  d
FT                   /number= exon 5
FT   exon            310..333
FT                   /*tag=  e
FT                   /number= exon 6
XX
PN   WO200185781-A2.
XX
PD   15-NOV-2001.
XX
PF   10-MAY-2001; 2001WO-GB02054.
XX
PR   10-MAY-2000; 2000GB-0011278.
XX
PA   (UNLO ) UNIV COLLEGE LONDON.
PA   (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
XX
PI   Goldspink G,  Terenghi G;
XX
DR   WPI; 2002-055585/07.
DR   P-PSDB; AAU10560.
XX
PT   Use of insulin-like growth factor I (IGF-I) isoform known as
PT   mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT   ability to reduce motoneuron loss in response to nerve avulsion, to
PT   treat nerve damage  -
XX
PS   Disclosure; Fig 6; 65pp; English.
XX
CC   The invention relates to the use of an insulin-like growth factor I
CC   (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC   of a medicament for treating nerve damage in the peripheral nervous
CC   system, or for treating nerve damage by localising MGF at the site of
CC   damage. The nerve damage may include severing of a nerve. The treatment
CC   may be combined with another treatment (such as a polypeptide growth
CC   factor other than MGF) that prevents or diminishes degeneration of the
CC   target organ (for example, muscle) which the damaged nerve innervates,
CC   whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC   MGF prevents or diminishes degeneration. The method is useful for
CC   treating neurological disorders, preferably motorneuron disorders. These
CC   methods can reduce motoneuron loss by 20% or greater in response to nerve
CC   avulsion. This sequence represents cDNA encoding the rat MGF.
XX
SQ   Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

  Query Match           68.2%;  Score 356.8;  DB 24;  Length 539;
  Best Local Similarity  82.3%;  Pred. No. 5.5e-95;
  Matches  436;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||| ||||||||||||||||||||
Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| |||||||||||||||| || |||||||||| |||||||||||| |||
Db         61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||
Db        121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              |||| | |  |||||| ||||| |||| || ||| |||| ||||||||||||||| |||
Db        181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  ||||| | ||| ||  ||||||||| ||||   || |||
Db        241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||| ||||||||||||||||||| ||||||||||||||| |||
Db        301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||     | || | || | ||||||| || ||||||
Db        361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||            |    |||||| |||| ||| ||||      || ||| ||||  ||
Db        421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530


RESULT 10
AAN70436
ID   AAN70436 standard; cDNA; 818 BP.
XX
AC   AAN70436;
XX
DT   05-APR-1991  (first entry)
XX
DE   Sequence encoding insulin-like growth factor 1A (IGF-1A).
XX
KW   Growth promoter; lactation enhancer;  cell proliferation; ss.
XX
OS   Homo sapiens.
XX
PN   EP229750-A.
XX
PD   22-JUL-1987.
XX
PF   06-JAN-1987;   87EP-0870001.
XX
PR   20-NOV-1986;   86US-0929671.
PR   07-JAN-1986;   86US-0816662.
XX
PA   (UNIW ) UNIV OF WASHINGTON.
XX
PI   Krivi GG,  Rotwein PS;
XX
DR   WPI; 1987-200203/29.
XX
PT   New pre-pro-insulin-like growth factor-1 protein - obtd. by
PT   recombinant DNA procedures for use as growth promoters for
PT   enhancing lactation, for stimulating cell proliferation etc.
XX
PS   Example; Fig 5; 59pp; English.
XX
CC   A 42 base oligonucleotide corresponding to the DNA sequence encoding
CC   amino acids 10 to 23 of mature human IGF-I was synthesized (AAN70437).
CC   The radiolabeled 42 mer was then employed to screen for IGF-I
CC   containing DNA sequences in a human liver cDNA library.  Insulin-
```

```
CC   like growth factors-1A and -1B cDNAs were isolated from a human cDNA
CC   library by using lambdagt 11 (AAN70435, AAN70436). The human IGF-1
CC   genomic gene was isolated and mapped. It encodes at least two
CC   preproinsulin-like growth factor-1 proteins. An essentially pure
CC   proproinsulin-like growth factor-1 protein comprising the sequence
CC   of amino acids shown in Figure six is claimed (AAP70277).
XX
SQ   Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other;

  Query Match           63.9%;  Score 334.4;  DB 8;  Length 818;
  Best Local Similarity  84.6%;  Pred. No. 2.6e-88;
  Matches  445;  Conservative    0;  Mismatches   26;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        203 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 262

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        263 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 322

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        323 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 382

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        383 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 442

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||
Db        443 ATGCCCAAGACCCAG---------------------------------------------- 457

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                  |||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        458 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 510

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| ||||||||||| ||||||
Db        511 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 570

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| |||||||| ||||| |||||| ||| ||||||||||||||||||| ||||
Db        571 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 630

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        631 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 676


RESULT 11
ABK84583
ID   ABK84583 standard; cDNA; 7260 BP.
XX
AC   ABK84583;
XX
DT   14-AUG-2002  (first entry)
XX
DE   Human cDNA differentially expressed in granulocytic cells #1154.
XX
KW   Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW   viral infection; parasitic infection; protozoal infection;
KW   fungal infection; sterile inflammatory disease; psoriasis;
KW   rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW   cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW   adult respiratory distress syndrome; inflammatory bowel disease;
KW   Crohn's disease; ulcerative colitis; periodontal disease;
KW   granulocyte activation; chronic inflammation; allergy.
XX
OS   Homo sapiens.
XX
PN   WO200228999-A2.
XX
PD   11-APR-2002.
XX
PF   03-OCT-2001; 2001WO-US30821.
XX
PR   03-OCT-2000; 2000US-237189P.
XX
PA   (GENE-) GENE LOGIC INC.
XX
PI   Beazer-Barclay Y,  Weissman SM,  Yamaga S,  Vockley J;
XX
DR   WPI; 2002-435328/46.
XX
PT   Detecting granulocyte activation by detecting differential expression
PT   of genes associated with granulocyte activation, which serves as
PT   diagnostic markers that is useful for monitoring disease states and
PT   drug toxicity -
XX
PS   Claim 1; SEQ ID No 1154; 114pp; English.
XX
CC   The invention relates to detecting (M1) granulocyte (GC) activation
CC   (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC   DNA chip analysis as given in the specification, and comparing
CC   the expression level to an unactivated
CC   GC, where differential expression of Gs is indicative of GCA.
CC   Also included are modulating (M2) GA by contacting GC with an agent
CC   that alters the expression of at least one gene in Gs; (2) screening (M3)
CC   for an agent capable of modulating GCA or an inflammation (especially
CC   chronic) in a tissue, an allergic response in a subject, exposure of a
CC   subject to a pathogen or sterile inflammatory disease using the
CC   gene expression profile; (3) detecting (M4) an inflammation (especially
CC   chronic) in a tissue, an allergic response in a subject, exposure of a
CC   subject to a pathogen or sterile inflammatory disease, by detecting the
CC   level of expression in a sample of the tissue of gene(s) from Gs, where
CC   the level of expression of the gene is indicative of inflammation;
CC   (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC   an allergic response in a subject, exposure of a subject to a pathogen
CC   or sterile inflammatory disease, by contacting a tissue having
CC   inflammation with an agent that modulates the expression of gene(s)
CC   from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC   modulating GA; M3 is useful for screening an agent capable of modulating
CC   GCA preferably in an inflammation in a tissue; M4 is useful for
CC   detecting an inflammation (especially chronic) in a tissue, an allergic
CC   response in a subject, exposure of a subject to a pathogen or sterile
CC   inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC   glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC   reperfusion injury, ARDS, adult respiratory distress syndrome,
CC   inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC   periodontal disease; also bacterial infection, viral infection,
CC   parasitic infection, protozoal infection, fungal infection and M5 is
CC   useful for treating one of the above conditions. The present
CC   sequence represents a gene differentially expressed in granulocytes.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

  Query Match           63.9%;  Score 334.4;  DB 24;  Length 7260;
  Best Local Similarity  84.6%;  Pred. No. 6.1e-88;
  Matches  445;  Conservative    0;  Mismatches   26;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
```

```
Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || ||||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||  |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                      |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| ||||||||||||||  |||| ||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| |||||||| ||||| |||||| |||  ||||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
```

RESULT 12
ABN97244
ID ABN97244 standard; DNA; 7260 BP.
XX
AC ABN97244;
XX
DT 13-AUG-2002 (first entry)
XX
DE Gene #3742 used to diagnose liver cancer.
XX
KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.
XX
OS Homo sapiens.
XX
PN WO200229103-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US30589.
XX
PR 02-OCT-2000; 2000US-237054P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;
XX
DR WPI; 2002-426119/45.
XX
PT Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample -
XX
PS Claim 1; SEQ ID NO 3742; 298pp; English.
XX
CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying,
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

```
  Query Match             63.9%;  Score 334.4;  DB 24;  Length 7260;
  Best Local Similarity   84.6%;  Pred. No. 6.1e-88;
  Matches  445;  Conservative    0;  Mismatches   26;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || ||||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||  |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                      |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| ||||||||||||||  |||| ||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| |||||||| ||||| |||||| |||  ||||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
```

RESULT 13
ABK64812
ID ABK64812 standard; DNA; 7260 BP.
XX
AC ABK64812;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human benign prostatic hyperplasia gene #707.
XX
KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200212440-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-US24708.
XX
PR 07-AUG-2000; 2000US-223323P.
PR 05-JUN-2001; 2001US-0873319.
XX
PA (GENE-) GENE LOGIC INC.

PA (NISB) JAPAN TOBACCO INC.
XX
PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
XX
DR WPI; 2002-257476/30.
XX
PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
PT cells -
XX
PS Disclosure; Page 391-393; 444pp; English.
XX
CC The invention relates to a method of diagnosing (I) the onset or
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
CC or identifying an agent that modulates the onset or progression of BPH.
CC The method is based on changes in gene expression in BPH tissue isolated
CC from patients exhibiting different clinical states of prostate
CC hyperplasia as compared to normal prostate tissue. (I) comprises
CC detecting the expression levels of one or more genes in prostate cells
CC from the subject that are differentially regulated compared to normal
CC prostate cells. (II) comprises preparing a first gene expression profile
CC of BPH cells or BPH-like cell population, exposing the cells to the
CC agent, preparing a second gene expression profile of the agent exposed
CC cells, and comparing the first and second gene expression profiles.
CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
CC useful for identifying an agent that modulates the onset or progression
CC of BPH. The methods are useful to present information identifying
CC the expression level in a tissue or cells, by comparing the expression
CC level of genes given in the specification in the tissue or cells to the
CC level of expression of gene in the database, and displaying the
CC expression levels of at least one gene in the tissue or cell sample
CC compared to the expression level in BPH. Agents using (II) are useful for
CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
CC benign prostatic hyperplasia gene sequences of the invention.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;
Best Local Similarity 84.6%; Pred. No. 6.1e-88;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| |||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| |||||||| ||||| |||||| ||| ||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
```

RESULT 14
ABK35504
ID ABK35504 standard; DNA; 7260 BP.
XX
AC ABK35504;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human endometrial cancer related gene, IGF1.
XX
KW Human; ds; gene; endometrial cancer; differential expression;
KW DNA microarray; protein microarray.
XX
OS Homo sapiens.
XX
PN WO200209573-A2.
XX
PD 07-FEB-2002.
XX
PF 31-JUL-2001; 2001WO-US24104.
XX
PR 31-JUL-2000; 2000US-221735P.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX
PI Mutter GL;
XX
DR WPI; 2002-179967/23.
DR P-PSDB; AAU84284.
XX
PT Diagnosing endometrial cancer comprises determining expression of
PT nucleic acid molecules or expression products that are differentially
PT expressed in normal and malignant endometrium -
XX
PS Claim 1; Page 85-89; 233pp; English.
XX
CC The invention relates to diagnosing endometrial cancer in a subject
CC suspected of having endometrial cancer comprising determining the
CC expression of a set of nucleic acid molecules or expression products in
CC an endometrial sample suspected of being cancerous, where the set of
CC nucleic acid molecules comprises at least 2 nucleic acid molecules
CC selected from 50 fully defined sequences as given in the specification.
CC The nucleic acids are used as an array of at least 2 of the 50
CC nucleic acids bound to a solid substrate. Also included is a solid-phase
CC protein microarray comprising at least 2 antibodies or its antigen
CC binding fragments, that specifically bind at least 2 different
CC polypeptides from the 50 fully defined sequences as given in the
CC specification, fixed to a solid substrate. The methods and arrays are
CC useful for the diagnosis of endometrial cancer, selecting and monitoring
CC treatment regimes and identification of lead compounds useful for the
CC treatment of endometrial cancer. The present sequence is one of 50
CC genes differentially expressed between cancerous and non-cancerous
CC samples.
XX
SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;
Best Local Similarity 84.6%; Pred. No. 6.1e-88;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430
```

```
Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                  |||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| ||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| ||| ||||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784


RESULT 15
ABK35561
ID   ABK35561 standard; DNA; 7260 BP.
XX
AC   ABK35561;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Gene IGF1 differentially expressed in breast cancer tissue.
XX
KW   Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
KW   MAI; mitotic activity index; cytostatic; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200210436-A2.
XX
PD   07-FEB-2002.
XX
PF   27-JUL-2001; 2001WO-US23642.
XX
PR   28-JUL-2000; 2000US-222093P.
XX
PA   (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
PA   (BAAK/) BAAK J.
XX
PI   Baak J,  Mutter GL;
XX
DR   WPI; 2002-180084/23.
DR   P-PSDB; AAU84341.
XX
PT   Diagnosing breast cancer comprises determining expression of nucleic
PT   acid molecules or expression products that are differentially expressed
PT   in normal and malignant tissue -
XX
PS   Claim 1; Page 74-78; 219pp; English.
XX
CC   The present invention relates to a method for diagnosing breast cancer
CC   in a subject suspected of having endometrial cancer. The method
CC   comprises determining the expression of a set of human genes or
CC   expression products in an endometrial sample suspected of being
CC   cancerous. The human genes of the invention are differentially
CC   expressed in breast tumours characterised as high or low MAI (mitotic
CC   activity index). These sets of genes can be used to discriminate between
CC   high and low MAI breast tumours. The invention also provides DNA and
CC   protein microarrays for analysing the expression of the human genes and
CC   their protein products. The methods and arrays are useful for the
CC   diagnosis and prognosis of endometrial cancer, selecting and monitoring
CC   treatment regimes, and identification of compounds useful for the
CC   treatment of endometrial cancer. ABK35531-ABK35581 represent the human
CC   genes of the invention that are differentially expressed in breast
CC   cancer tissue.
XX
SQ   Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

  Query Match             63.9%;  Score 334.4;  DB 24;  Length 7260;
  Best Local Similarity   84.6%;  Pred. No. 6.1e-88;
  Matches  445;  Conservative    0;  Mismatches   26;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                  |||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| ||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| ||| ||||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784


Search completed: June 15, 2003, 16:08:51
Job time : 160.655 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:46:38 ; Search time 42.3965 Seconds
(without alignments)
3783.145 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	523	100.0	553	4	US-09-142-583A-3	Sequence 3, Appli
2	523	100.0	553	4	US-09-142-583A-5	Sequence 5, Appli
3	332.8	63.6	777	4	US-09-142-583A-10	Sequence 10, Appl
4	331.2	63.3	622	6	5405942-2	Patent No. 5405942
5	274.6	52.5	5707	2	US-08-472-809B-8	Sequence 8, Appli
6	274.6	52.5	6345	2	US-08-472-809B-7	Sequence 7, Appli
7	234.4	44.8	357	6	5405942-13	Patent No. 5405942
8	232.8	44.5	357	6	5405942-9	Patent No. 5405942
9	191.4	36.6	210	6	5405942-7	Patent No. 5405942
10	191.4	36.6	210	6	5405942-11	Patent No. 5405942
11	191.4	36.6	2862	4	US-09-255-829-13	Sequence 13, Appl
12	189.8	36.3	210	6	5405942-15	Patent No. 5405942
13	185.2	35.4	240	1	US-08-308-196A-1	Sequence 1, Appli
14	185.2	35.4	240	5	PCT-US91-06452-1	Sequence 1, Appli
15	185.2	35.4	390	3	US-09-029-267-13	Sequence 13, Appl
16	158.8	30.4	798	1	US-07-953-230A-6	Sequence 6, Appli
17	154.8	29.6	770	1	US-07-953-230A-1	Sequence 1, Appli
18	154.8	29.6	846	1	US-07-953-230A-5	Sequence 5, Appli
19	127	24.3	621	3	US-08-989-251-40	Sequence 40, Appl
20	127	24.3	621	3	US-09-340-250-40	Sequence 40, Appl
21	127	24.3	621	4	US-09-528-108-40	Sequence 40, Appl
22	125.8	24.1	233	1	US-08-444-142-3	Sequence 3, Appli
23	125.8	24.1	233	1	US-08-444-131-3	Sequence 3, Appli
24	125.8	24.1	485	1	US-07-989-845-29	Sequence 29, Appl
25	125.8	24.1	485	1	US-07-989-844-13	Sequence 13, Appl
26	125.8	24.1	485	1	US-08-110-663-1	Sequence 1, Appli
27	125.8	24.1	485	1	US-08-169-688-1	Sequence 1, Appli
28	125.8	24.1	485	1	US-08-240-121-13	Sequence 13, Appl
29	125.8	24.1	485	1	US-08-451-241-13	Sequence 13, Appl
30	125.8	24.1	485	1	US-08-110-664-1	Sequence 1, Appli
31	125.8	24.1	485	1	US-08-446-882-1	Sequence 1, Appli
32	125.8	24.1	485	1	US-08-385-187A-1	Sequence 1, Appli
33	125.8	24.1	485	1	US-08-470-108-1	Sequence 1, Appli
34	125.8	24.1	485	5	PCT-US93-11297-13	Sequence 13, Appl
35	125.8	24.1	485	5	PCT-US93-11298-29	Sequence 29, Appl
36	125.6	24.0	243	2	US-08-482-182-75	Sequence 75, Appl
37	124.2	23.7	717	1	US-08-284-784-40	Sequence 40, Appl
38	124.2	23.7	717	2	US-08-854-811-40	Sequence 40, Appl
39	124.2	23.7	783	1	US-08-284-784-43	Sequence 43, Appl
40	124.2	23.7	783	2	US-08-854-811-43	Sequence 43, Appl
41	124.2	23.7	891	1	US-08-284-784-33	Sequence 33, Appl
42	124.2	23.7	891	1	US-08-284-784-34	Sequence 34, Appl
43	124.2	23.7	891	2	US-08-854-811-33	Sequence 33, Appl
44	124.2	23.7	891	2	US-08-854-811-34	Sequence 34, Appl
45	124.2	23.7	900	1	US-08-284-784-24	Sequence 24, Appl

ALIGNMENTS

```
RESULT 1
US-09-142-583A-3
; Sequence 3, Application US/09142583A
; Patent No. 6221842
;   GENERAL INFORMATION:
;        APPLICANT: GOLDSPINK, GEOFFREY
;        TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22201
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/142,583A
;             FILING DATE: 29-Oct-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: WO PCT/GB97/00658
;             FILING DATE: 11-MAR-1997
;             APPLICATION NUMBER: GB 9605124.8
;             FILING DATE: 11-MAR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SADOFF, B. J.
;             REGISTRATION NUMBER: 36663
;             REFERENCE/DOCKET NUMBER: 117-263
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 7038164000
;             TELEFAX: 7038164100
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 553 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: both
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION: 1..363
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-142-583A-3

  Query Match             100.0%;  Score 523;  DB 4;  Length 553;
```

```
  Best Local Similarity   100.0%;  Pred. No. 1.3e-154;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATTT 510

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        511 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553


RESULT 2
US-09-142-583A-5
; Sequence 5, Application US/09142583A
; Patent No. 6221842
;   GENERAL INFORMATION:
;        APPLICANT: GOLDSPINK, GEOFFREY
;        TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22201
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/142,583A
;             FILING DATE: 29-Oct-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: WO PCT/GB97/00658
;             FILING DATE: 11-MAR-1997
;             APPLICATION NUMBER: GB 9605124.8
;             FILING DATE: 11-MAR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SADOFF, B. J.
;             REGISTRATION NUMBER: 36663
;             REFERENCE/DOCKET NUMBER: 117-263
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 7038164000
;             TELEFAX: 7038164100
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 553 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: both
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION: 341..397
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-142-583A-5

  Query Match             100.0%;  Score 523;  DB 4;  Length 553;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-154;
  Matches  523;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATTT 510

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        511 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553


RESULT 3
US-09-142-583A-10
; Sequence 10, Application US/09142583A
; Patent No. 6221842
;   GENERAL INFORMATION:
;        APPLICANT: GOLDSPINK, GEOFFREY
;        TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
;        NUMBER OF SEQUENCES: 11
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: NIXON & VANDERHYE P.C.
;             STREET: 1100 NORTH GLEBE ROAD
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22201
;        COMPUTER READABLE FORM:
```

```
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/142,583A
;             FILING DATE: 29-Oct-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: WO PCT/GB97/00658
;             FILING DATE: 11-MAR-1997
;             APPLICATION NUMBER: GB 9605124.8
;             FILING DATE: 11-MAR-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SADOFF, B. J.
;             REGISTRATION NUMBER: 36663
;             REFERENCE/DOCKET NUMBER: 117-263
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 7038164000
;             TELEFAX: 7038164100
;    INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 777 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: both
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION: 26..493
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-142-583A-10

  Query Match             63.6%;  Score 332.8;  DB 4;  Length 777;
  Best Local Similarity   84.4%;  Pred. No. 7.7e-95;
  Matches  444;  Conservative    0;  Mismatches   27;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        179 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 238

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        239 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 298

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        299 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 358

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||
Db        359 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 418

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||
Db        419 ATGCCCAAGACCCAG---------------------------------------------- 433

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                  |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        434 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 486

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| ||||||||||||  |||| |||||||||||| ||||||
Db        487 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 546

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| ||| ||||||||||||||||||| ||||
Db        547 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 606

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        607 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 652
```

```
RESULT 4
5405942-2
;Patent No. 5405942
;    APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;    NUMBER OF SEQUENCES: 16
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/65,673
;      FILING DATE: 16-JUN-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 630,557
;      FILING DATE: 19-JUL-1984
;SEQ ID NO:2:
;      LENGTH: 622
5405942-2

  Query Match             63.3%;  Score 331.2;  DB 6;  Length 622;
  Best Local Similarity   68.3%;  Pred. No. 2.2e-94;
  Matches  359;  Conservative   84;  Mismatches   28;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||:|:|||| ||:||||:||:|||:||:|:::|||:::||:|:|:||||||
Db         45 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 104

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||:::|:::|||||||||||||||| :| |||:|||||||:|||||||| ||:|||
Db        105 AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 164

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||| |:||:|||:|||:||:|:|::||||||:|:|:|:  |||||||:||||||:|:|
Db        165 ACAGGUAUCGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCAUAGGAGGCUGGAGAUGUAU 224

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              :| |||||||:|||||| || ||| |||| |||:| |:|||:||||||||||||||||||
Db        225 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGCUCUGUCCGUGCCCAGCGCCACACCGAC 284

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |:|||||||||  |||
Db        285 AUGCCCAAGACCCAG---------------------------------------------- 299

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                  |||||||:|||:::|||||||  ||||:|||||||:|||||||||||||||:|
Db        300 -------AAGGAAGUACAUUUGAAGAACGCAAGUAGAGGGAGUGCAGGAAACAAGAACUA 352

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||:|:|||||||||||: |:|||||||:|||||  |||| ||||||||||| ||:::|
Db        353 CAGGAUGUAGGAAGACCCUCCUGAGGAGUGAAGAGUGACAUGCCACCGCAGGAUCCUUUG 412

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |:|:|||| ||::|||:| :|||| ::||||  |||  ||||||||:|||:::||: |||:
Db        413 CUCUGCACGAGUUACCUGUUAAACUUUGGAACACCUACCAAAAAAUAAGUUUGAUAACAU 472

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              :: |||||: ||| :::|||||||:||||:|||||||:|||||::|
Db        473 UUAAAAGAUGGGCGUUUCCCCCAAUGAAAUACACAAGUAAACAUUC 518
```

```
RESULT 5
US-08-472-809B-8
; Sequence 8, Application US/08472809B
; Patent No. 5925564
;  GENERAL INFORMATION:
;    APPLICANT:  Schwartz, Robert J.
;    APPLICANT:  DeMayo, Franco J.
;    APPLICANT:  O'Malley, Bert W.
;    TITLE OF INVENTION:  Expression Vector Systems and
;    TITLE OF INVENTION:  Method of Use
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
```

```
;       STREET:  633 West Fifth Street
;       STREET:  Suite 4700
;       CITY:  Los Angeles
;       STATE:  California
;       COUNTRY:  U.S.A.
;       ZIP:  90071-2066
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;       MEDIUM TYPE:  storage
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  IBM P.C. DOS 5.0
;       SOFTWARE:  Word Perfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/472,809B
;       FILING DATE:  June 7, 1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/209,846
;       FILING DATE:  March 9, 1994
;       APPLICATION NUMBER:  07/789,919
;       FILING DATE:  No. 5925564ember 6, 1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard J.
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  214/212
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213) 955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5707 bases
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-472-809B-8

  Query Match             52.5%;  Score 274.6;  DB 2;  Length 5707;
  Best Local Similarity   82.2%;  Pred. No. 4.1e-76;
  Matches  351;  Conservative    0;  Mismatches   24;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        793 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 852

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        853 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 912

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        913 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 972

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || ||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        973 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 1032

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||| |||
Db       1033 ATGCCCAAGACCCAG---------------------------------------------- 1047

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                      |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1048 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 1100

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||   |||| ||||||||||| ||    |
Db       1101 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCG 1160

Qy        421 CTCTGCA 427
                |||||
Db       1161 GGCTGCA 1167
```

```
RESULT 6
US-08-472-809B-7
; Sequence 7, Application US/08472809B
; Patent No. 5925564
;  GENERAL INFORMATION:
;    APPLICANT:  Schwartz, Robert J.
;    APPLICANT:  DeMayo, Franco J.
;    APPLICANT:  O'Malley, Bert W.
;    TITLE OF INVENTION:  Expression Vector Systems and
;    TITLE OF INVENTION:  Method of Use
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/472,809B
;      FILING DATE:  June 7, 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/209,846
;      FILING DATE:  March 9, 1994
;      APPLICATION NUMBER:  07/789,919
;      FILING DATE:  No. 5925564ember 6, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  214/212
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6345 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-472-809B-7

  Query Match             52.5%;  Score 274.6;  DB 2;  Length 6345;
  Best Local Similarity   82.2%;  Pred. No. 4.3e-76;
  Matches  351;  Conservative    0;  Mismatches   24;  Indels   52;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       3702 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 3761

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db       3762 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 3821

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       3822 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 3881

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || ||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db       3882 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 3941
```

```
Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||| |||
Db       3942 ATGCCCAAGACCCAG---------------------------------------------- 3956

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       3957 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 4009

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| ||||||||||| ||    |
Db       4010 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCG 4069

Qy        421 CTCTGCA 427
              |||||
Db       4070 GGCTGCA 4076


RESULT 7
5405942-13
;Patent No. 5405942
;    APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;    NUMBER OF SEQUENCES: 16
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/65,673
;      FILING DATE: 16-JUN-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 630,557
;      FILING DATE: 19-JUL-1984
;SEQ ID NO:13:
;      LENGTH: 357
5405942-13

  Query Match             44.8%;  Score 234.4;  DB 6;  Length 357;
  Best Local Similarity   93.8%;  Pred. No. 3.9e-64;
  Matches  244;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         43 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 102

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        103 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 162

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||| |||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        163 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 222

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||| ||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        223 TGCGCACCCCTCAGGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 282

Qy        241 ATGCCCAAGACTCAGAAGTA 260
              |||||||||||| |||||| |
Db        283 ATGCCCAAGACCCAGAAGGA 302


RESULT 8
5405942-9
;Patent No. 5405942
;    APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;    NUMBER OF SEQUENCES: 16
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/65,673
;      FILING DATE: 16-JUN-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 630,557
;      FILING DATE: 19-JUL-1984
;SEQ ID NO:9:
;      LENGTH: 357
5405942-9

  Query Match             44.5%;  Score 232.8;  DB 6;  Length 357;
  Best Local Similarity   76.5%;  Pred. No. 1.2e-63;
  Matches  199;  Conservative   44;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||:|:|||| ||:||||:||:||| ||:|:::|||::||:|:|:|||||
Db         43 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGACGCUCUUCAGUUCGUGUGUGGAGAC 102

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||::::|:::|||||||||||||||| :| |||:|||||||:|||||||| ||:|||
Db        103 AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 162

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||| |:||:|||:|||:||:| ::|||||||:|:||:|: |||||||:|||||:|:|
Db        163 ACAGGUAUCGUGGAUGAGUGCUGUUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 222

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              :| |||||||:|||||| || ||| |||| |||:| |:|||:|||||||||||||||||||
Db        223 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGCUCUGUCCGUGCCCAGCGCCACACCGAC 282

Qy        241 ATGCCCAAGACTCAGAAGTA 260
              |:|||||||||| |||||| |
Db        283 AUGCCCAAGACCCAGAAGGA 302


RESULT 9
5405942-7
;Patent No. 5405942
;    APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;    NUMBER OF SEQUENCES: 16
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/65,673
;      FILING DATE: 16-JUN-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 630,557
;      FILING DATE: 19-JUL-1984
;SEQ ID NO:7:
;      LENGTH: 210
5405942-7

  Query Match             36.6%;  Score 191.4;  DB 6;  Length 210;
  Best Local Similarity   75.1%;  Pred. No. 9.1e-51;
  Matches  157;  Conservative   41;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||:|:|||| ||:||||:||:||| ||:|:::|||::||:|:|:|||||
Db          1 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||::::|:::|||||||||||||||| :| |||:|||||||:|||||||| ||:|||
Db         61 AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||| |:||:|||:|||:||:|::|||||||:|:||:|: |||||||:|||||:|:|
Db        121 ACAGGUAUCGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
              :| |||||||:|||||| || ||| ||||
Db        181 UGCGCACCCCUCAAGCCUGCCAAGUCAGC 209


RESULT 10
5405942-11
;Patent No. 5405942
;    APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
```

```
;JAMES P.
;    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;    NUMBER OF SEQUENCES: 16
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/65,673
;      FILING DATE: 16-JUN-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 630,557
;      FILING DATE: 19-JUL-1984
;SEQ ID NO:11:
;      LENGTH: 210
5405942-11

  Query Match            36.6%;  Score 191.4;  DB 6;  Length 210;
  Best Local Similarity   94.7%;  Pred. No. 9.1e-51;
  Matches  198;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||  |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
              || |||||||||||||| || ||| ||||
Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGC 209


RESULT 11
US-09-255-829-13
; Sequence 13, Application US/09255829
; Patent No. 6461617
;  GENERAL INFORMATION:
;    APPLICANT:  Shone, Clifford Charles
;    APPLICANT:  Quinn, Conrad Padraig
;    APPLICANT:  Foster, Keith Alan
;    TITLE OF INVENTION:  Recombinant Toxin Fragments
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
;      STREET:  1100 NEW YORK AVENUE, NW, SUITE 600
;      CITY:  WASHINGTON
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/255,829
;      FILING DATE:  23-FEB-1999
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB97/02273
;      FILING DATE:  22-AUG-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/782,893
;      FILING DATE:  27-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ESMOND, ROBERT W.
;      REGISTRATION NUMBER:  32,893
;      REFERENCE/DOCKET NUMBER:  1581.0130002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2540
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2862 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2862
US-09-255-829-13

  Query Match            36.6%;  Score 191.4;  DB 4;  Length 2862;
  Best Local Similarity   94.7%;  Pred. No. 3.6e-50;
  Matches  198;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       2644 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 2703

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||||||||| ||||||
Db       2704 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 2763

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||  |||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       2764 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 2823

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
              || |||||||||||||| || ||| ||||
Db       2824 TGCGCACCCCTCAAGCCTGCCAAGTCAGC 2852


RESULT 12
5405942-15
;Patent No. 5405942
;    APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;    TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;    NUMBER OF SEQUENCES: 16
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/65,673
;      FILING DATE: 16-JUN-1987
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 630,557
;      FILING DATE: 19-JUL-1984
;SEQ ID NO:15:
;      LENGTH: 210
5405942-15

  Query Match            36.3%;  Score 189.8;  DB 6;  Length 210;
  Best Local Similarity   74.6%;  Pred. No. 2.9e-50;
  Matches  156;  Conservative   41;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||:|:|||| ||:||||:||:|||:||:|:::|||::||:|:|:||||||
Db          1 GGACCGGAGACGCUCUGCGGGGCUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||::::|:::|||||||||||||||| :| |||:|||||||:|||||||| ||:|||
Db         61 AGGGGCUUUUAUUUCAACAAGCCCACAGGGUAUGGCUCCAGCAGUCGGAGGGCGCCUCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||  |:||:|||:|||:||::||||||||:|:||:|: |||||||:|||||:|:|
Db        121 ACAGGUAUCGUGGAUGAGUGCUGCUUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
              :| ||||||||:|| ||| || ||| ||||
Db        181 UGCGCACCCCUCAGGCCUGCCAAGUCAGC 209


RESULT 13
```

```
US-08-308-196A-1
; Sequence 1, Application US/08308196A
; Patent No. 5612198
;  GENERAL INFORMATION:
;    APPLICANT:  Brierley, Russell A.
;    APPLICANT:  Davis, Geneva R.
;    APPLICANT:  Holtz, Gregory C.
;    APPLICANT:  Gleeson, Martin A.
;    APPLICANT:  Howard, Bradley D.
;    TITLE OF INVENTION:  Production of Insulin-Like Growth
;    TITLE OF INVENTION:  Factor-1 in Methylotrophic Yeast Cells
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/308,196A
;      FILING DATE:  09-SEPT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/983,523
;      FILING DATE:  03-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/578,728
;      FILING DATE:  04-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  51875
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  14..232
US-08-308-196A-1

  Query Match           35.4%;  Score 185.2;  DB 1;  Length 240;
  Best Local Similarity   91.6%;  Pred. No. 8.6e-49;
  Matches  196;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||| |||||||||| ||||||||||||||||||||
Db         17 GGACCGGAGACGCTCTGCGGGGCTGAGCTCGTGGATGCTCTGCAGTTCGTGTGTGGAGAC 76

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||||| || ||||||||||||||  |||| ||||||
Db         77 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 136

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||
Db        137 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 196

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCT 214
              || |||||||||||||| || ||| ||||  | |
Db        197 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 230
```

```
RESULT 14
PCT-US91-06452-1
; Sequence 1, Application PC/TUS9106452
;  GENERAL INFORMATION:
;    APPLICANT:  Brierley, Russell A.
;    APPLICANT:  Davis, Geneva R.
;    APPLICANT:  Holtz, Gregory C.
;    APPLICANT:  Gleeson, Martin A.
;    APPLICANT:  Bradley, D. H.
;    TITLE OF INVENTION:  Production of Insulin-Like Growth
;    TITLE OF INVENTION:  Factor-1 in Methylotrophic Yeast Cells
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fitch, Even, Tabin & Flannery
;      STREET:  135 South LaSalle Street, Suite 900
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/06452
;      FILING DATE:  19910409
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/578,728
;      FILING DATE:  04-SEP-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  51874
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)552-1311
;      TELEFAX:  (619)552-0095
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  240 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  14..232
PCT-US91-06452-1

  Query Match           35.4%;  Score 185.2;  DB 5;  Length 240;
  Best Local Similarity   91.6%;  Pred. No. 8.6e-49;
  Matches  196;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||| |||||||||| ||||||||||||||||||||
Db         17 GGACCGGAGACGCTCTGCGGGGCTGAGCTCGTGGATGCTCTGCAGTTCGTGTGTGGAGAC 76

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||||| || ||||||||||||||  |||| ||||||
Db         77 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 136

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||| ||||||||
Db        137 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 196

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCT 214
              || |||||||||||||| || ||| ||||  | |
Db        197 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 230


RESULT 15
US-09-029-267-13
```

```
; Sequence 13, Application US/09029267
; Patent No. 6107057
;  GENERAL INFORMATION:
;    APPLICANT:  Crawford, Kenneth
;    APPLICANT:  Zaror, Isabel
;    APPLICANT:  Innis, Michael
;    TITLE OF INVENTION:  Pichia Secretory Leader for Protein
;    TITLE OF INVENTION:  Expression
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  94608
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/029,267
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Chung, Ling-Fong
;      REGISTRATION NUMBER:  36,482
;      REFERENCE/DOCKET NUMBER:  1165.100
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2704
;      TELEFAX:  (510) 655-3542
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  390 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "Synthetic"
US-09-029-267-13

  Query Match           35.4%;  Score 185.2;  DB 3;  Length 390;
  Best Local Similarity  91.6%;  Pred. No. 1.1e-48;
  Matches  196;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||| |||||||||| ||||||||||||||||||
Db        160 GGACCGGAGACGCTCTGCGGGGCTGAGCTCGTGGATGCTCTGCAGTTCGTGTGTGGAGAC 219

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || |||||||||||||  |||| ||||||
Db        220 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 279

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||
Db        280 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 339

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCT 214
              || |||||||||||||| || ||| |||| | |
Db        340 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 373


Search completed: June 15, 2003, 18:20:42
Job time : 43.3965 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 17:22:19 ; Search time 94.7296 Seconds
(without alignments)
7994.713 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	523	100.0	523	10	US-09-852-261-5	Sequence 5, Appli
2	467.4	89.4	517	10	US-09-852-261-1	Sequence 1, Appli
3	409	78.2	471	10	US-09-852-261-13	Sequence 13, Appl
4	356.8	68.2	539	10	US-09-852-261-3	Sequence 3, Appli
5	349.4	66.8	651	9	US-10-161-088-1	Sequence 1, Appli
6	334.4	63.9	7260	9	US-10-136-639-4	Sequence 4, Appli
7	334.4	63.9	7260	10	US-09-919-497-24	Sequence 24, Appl
8	334.4	63.9	7260	10	US-09-880-107-3739	Sequence 3739, Ap
9	262	50.1	487	10	US-09-852-261-11	Sequence 11, Appl
10	237.6	45.4	318	10	US-09-852-261-9	Sequence 9, Appli
11	228	43.6	462	9	US-10-238-114-1	Sequence 1, Appli
12	209	40.0	286	9	US-10-161-088-3	Sequence 3, Appli
13	187	35.8	4532	10	US-09-930-377B-1	Sequence 1, Appli
14	186.6	35.7	210	10	US-09-930-377B-2	Sequence 2, Appli
15	185.2	35.4	390	9	US-10-179-046-13	Sequence 13, Appl
16	141.6	27.1	213	9	US-10-076-816-9	Sequence 9, Appli
17	141.6	27.1	213	9	US-10-077-381-9	Sequence 9, Appli
18	127	24.3	621	9	US-10-280-826-40	Sequence 40, Appl
19	127	24.3	621	10	US-09-921-398-40	Sequence 40, Appl
20	113.4	21.7	480	9	US-10-280-826-38	Sequence 38, Appl
21	113.4	21.7	480	10	US-09-921-398-38	Sequence 38, Appl
22	77.2	14.8	854	9	US-09-954-531-989	Sequence 989, App
c 23	75.4	14.4	447	9	US-10-025-380-917	Sequence 917, App
c 24	75.4	14.4	447	10	US-09-922-217-917	Sequence 917, App
c 25	75.4	14.4	447	10	US-09-833-263-917	Sequence 917, App
c 26	75.2	14.4	437	9	US-10-066-543-663	Sequence 663, App
c 27	75.2	14.4	493	9	US-10-066-543-997	Sequence 997, App
c 28	75.2	14.4	518	9	US-10-066-543-1040	Sequence 1040, Ap
c 29	75.2	14.4	536	9	US-10-066-543-428	Sequence 428, App
30	75.2	14.4	543	9	US-10-136-841-1	Sequence 1, Appli
c 31	75.2	14.4	549	9	US-10-066-543-478	Sequence 478, App
c 32	75.2	14.4	574	9	US-10-025-380-918	Sequence 918, App
c 33	75.2	14.4	574	10	US-09-922-217-918	Sequence 918, App
c 34	75.2	14.4	574	10	US-09-833-263-918	Sequence 918, App
c 35	75.2	14.4	577	9	US-10-066-543-1137	Sequence 1137, Ap
c 36	75.2	14.4	579	9	US-10-066-543-1094	Sequence 1094, Ap
c 37	75.2	14.4	586	9	US-10-066-543-808	Sequence 808, App
38	75.2	14.4	1356	9	US-10-081-119-37	Sequence 37, Appl
39	75.2	14.4	1356	9	US-10-097-340-144	Sequence 144, App
40	75.2	14.4	1356	10	US-09-962-436-293	Sequence 293, App
41	75.2	14.4	1356	10	US-09-954-456-294	Sequence 294, App
42	75.2	14.4	1356	10	US-09-880-107-2092	Sequence 2092, Ap
43	75.2	14.4	4350	9	US-10-125-181-37	Sequence 37, Appl
44	73.8	14.1	411	10	US-09-960-352-2082	Sequence 2082, Ap
45	72	13.8	237	9	US-10-136-841-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-852-261-5
; Sequence 5, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPINK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-09-852-261-5

Query Match 100.0%; Score 523; DB 10; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.2e-163;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
```

```
Db        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATTT 480

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
```

RESULT 2
US-09-852-261-1
; Sequence 1, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPINK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-261-1

Query Match 89.4%; Score 467.4; DB 10; Length 517;
Best Local Similarity 96.2%; Pred. No. 3.7e-145;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| |||| ||||||||||||||||||||||||
Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||| |||||||||||||| |||||||||||||||| | |||||||| |
Db        241 ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
```

```
Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATTT 476

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 521
              |||||||||||||||||||||||||||||||||||||||||
Db        477 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACAT 517
```

RESULT 3
US-09-852-261-13
; Sequence 13, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPINK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-09-852-261-13

Query Match 78.2%; Score 409; DB 10; Length 471;
Best Local Similarity 90.1%; Pred. No. 9.6e-126;
Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGCCCAAGACTCAG----------------------------------------------- 255

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 -------AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATTT 428

Qy        481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||||||||||||||||||||||||||||||||||||||
Db        429 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 471
```

RESULT 4
US-09-852-261-3

```
; Sequence 3, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDSPINK, GEOFFREY
;  APPLICANT:  TERENGHI, GIORGIO
;  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;  FILE REFERENCE: 117-351
;  CURRENT APPLICATION NUMBER: US/09/852,261
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: GB 0011278.9
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 539
;   TYPE: DNA
;   ORGANISM: Rattus sp.
US-09-852-261-3

  Query Match             68.2%;  Score 356.8;  DB 10;  Length 539;
  Best Local Similarity   82.3%;  Pred. No. 2.4e-108;
  Matches  436;  Conservative    0;  Mismatches   87;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||| ||||||||||||||||||||||
Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| ||||||||||||||| || |||||||||| ||||||||||||||||||
Db         61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||  | |  ||||||  |||||  |||| || |||  |||| ||||||||||||||  |||
Db        181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||  |||||  | |||  ||  |||||||| ||||    ||  |||
Db        241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||  ||||||||||||||||||||  ||||||||||||||||  |||
Db        301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||  |||||||| || |||  | |||||    |  || |  || |  ||||||| || ||||||
Db        361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||          |    ||||||  |||| |||  ||||      || |||  ||||  ||
Db        421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              |||||||  |||| ||||||||||  ||||||||||||||||||||||||
Db        481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 530


RESULT 5
US-10-161-088-1
; Sequence 1, Application US/10161088
; Publication No. US20030077761A1
; GENERAL INFORMATION:
;  APPLICANT: Parrow, Vendela
;  APPLICANT:  Rosengren, Linda
;  TITLE OF INVENTION: NEW METHODS
;  FILE REFERENCE: 13425-111001
;  CURRENT APPLICATION NUMBER: US/10/161,088
;  CURRENT FILING DATE:  2002-05-31
;  PRIOR APPLICATION NUMBER: SE 0101934-8
;  PRIOR FILING DATE: 2001-06-01
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 651
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (73)...(471)
US-10-161-088-1

  Query Match             66.8%;  Score 349.4;  DB 9;  Length 651;
  Best Local Similarity   82.8%;  Pred. No. 7.8e-106;
  Matches  425;  Conservative    0;  Mismatches   81;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||||
Db        139 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 198

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||||
Db        199 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 258

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| ||||||||||||||||||||||||||| ||||||||||||
Db        259 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  |||| ||||||||||  ||||||||||||||||||  |||
Db        319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 378

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        379 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| |  ||||   | || | ||  ||||||||||| ||||||
Db        499 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 558

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||          |    ||||||  | || |||  |||       || |||||||   ||
Db        559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAA 506
              |||||  ||||||| ||||||||||||||||||
Db        619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651


RESULT 6
US-10-136-639-4
; Sequence 4, Application US/10136639
; Publication No. US20030072761A1
; GENERAL INFORMATION:
;  APPLICANT: LeBowitz, Jonathan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS THE BLO
;  TITLE OF INVENTION:  BARRIER
;  FILE REFERENCE: SYM-008
;  CURRENT APPLICATION NUMBER: US/10/136,639
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US 60/329,650
;  PRIOR FILING DATE: 2001-10-16
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 7260
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-136-639-4
```

```
  Query Match           63.9%;  Score 334.4;  DB 9;  Length 7260;
  Best Local Similarity  84.6%;  Pred. No. 2.8e-100;
  Matches  445;  Conservative    0;  Mismatches   26;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || ||||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                      |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| ||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  |||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784


RESULT 7
US-09-919-497-24
; Sequence 24, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
;  APPLICANT: Mutter, George L.
;  TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
;  FILE REFERENCE: B0801/7225
;  CURRENT APPLICATION NUMBER: US/09/919,497
;  CURRENT FILING DATE:  2001-07-31
;  PRIOR APPLICATION NUMBER: US 60/221,735
;  PRIOR FILING DATE: 2000-07-31
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
;   LENGTH: 7260
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-919-497-24

  Query Match           63.9%;  Score 334.4;  DB 10;  Length 7260;
  Best Local Similarity  84.6%;  Pred. No. 2.8e-100;
  Matches  445;  Conservative    0;  Mismatches   26;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || ||||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                      |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| ||||||||||| ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| ||||||||| ||||| |||||| |||  |||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784


RESULT 8
US-09-880-107-3739
; Sequence 3739, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,379
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3739
;   LENGTH: 7260
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025
US-09-880-107-3739

  Query Match           63.9%;  Score 334.4;  DB 10;  Length 7260;
  Best Local Similarity  84.6%;  Pred. No. 2.8e-100;
  Matches  445;  Conservative    0;  Mismatches   26;  Indels   55;  Gaps    4;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db        371 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
```

```
Db        491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 550

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||| |||
Db        551 ATGCCCAAGACCCAG---------------------------------------------- 565

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        566 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||  |||| ||||||||||||  ||||||
Db        619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACAT 478
              |||||||| |||||||| ||||| |||||| |||  ||||||||||||||||| ||||
Db        679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||
Db        739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784


RESULT 9
US-09-852-261-11
; Sequence 11, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDSPINK, GEOFFREY
;  APPLICANT:  TERENGHI, GIORGIO
;  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;  FILE REFERENCE: 117-351
;  CURRENT APPLICATION NUMBER: US/09/852,261
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: GB 0011278.9
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 487
;   TYPE: DNA
;   ORGANISM: Rattus sp.
US-09-852-261-11

  Query Match             50.1%;  Score 262;  DB 10;  Length 487;
  Best Local Similarity   74.7%;  Pred. No. 8.1e-77;
  Matches  396;  Conservative    0;  Mismatches   75;  Indels   59;  Gaps    3;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| |||||||||||||| ||||||||||||||||||||||||
Db          1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| ||||||||||||||  || |||||||||  |||||||||||  |||
Db         61 AGGGGCTTTTACTTCAACAAGCCCACAGTCTATGGCTCCAGCATTCGGAGGGCACCACAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              || ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        121 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||  | |  ||||||  ||||| |||| || ||| |||| ||||||||||||| |||
Db        181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              ||||||||||||||||
Db        241 ATGCCCAAGACTCAG---------------------------------------------- 255

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||| |||||||||||||||||||| |||||||||||||||| |||
Db        256 -------AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 308

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| | |||||     | || | || | |||||||| || ||||||
Db        309 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 368

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||           |     |||||| |||| ||| ||||       || ||| ||||  ||
Db        369 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 428

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              ||||||| |||| |||||||||| ||||||||||||||||||||||||
Db        429 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 478


RESULT 10
US-09-852-261-9
; Sequence 9, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDSPINK, GEOFFREY
;  APPLICANT:  TERENGHI, GIORGIO
;  TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;  FILE REFERENCE: 117-351
;  CURRENT APPLICATION NUMBER: US/09/852,261
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: GB 0011278.9
;  PRIOR FILING DATE: 2000-05-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 318
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-852-261-9

  Query Match             45.4%;  Score 237.6;  DB 10;  Length 318;
  Best Local Similarity   94.6%;  Pred. No. 8.5e-69;
  Matches  246;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||||| || ||||||||||||||||||| ||||||
Db         61 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| |||| ||||||||||||||||||||||||||
Db        181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240

Qy        241 ATGCCCAAGACTCAGAAGTA 260
              |||||||||| |||||| |
Db        241 ATGCCCAAGACCCAGAAGGA 260


RESULT 11
US-10-238-114-1
; Sequence 1, Application US/10238114
; Publication No. US20030100073A1
; GENERAL INFORMATION:
;  APPLICANT: Merial
;  APPLICANT:  ANDREONI , Christine Michele
;  TITLE OF INVENTION: IGF-1 AS FELINE VACCINE ADJUVANT, IN PARTICULAR AGAINST FELINE
;  FILE REFERENCE: 454313-3165.1
;  CURRENT APPLICATION NUMBER: US/10/238,114
;  CURRENT FILING DATE:  2002-09-10
;  PRIOR APPLICATION NUMBER: FR 01 11736
;  PRIOR FILING DATE: 2001-09-11
;  PRIOR APPLICATION NUMBER: US 60/318,666
```

```
;  PRIOR FILING DATE: 2001-09-12
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 462
;   TYPE: DNA
;   ORGANISM: Felis catus
US-10-238-114-1

  Query Match            43.6%;  Score 228;  DB 9;  Length 462;
  Best Local Similarity   92.3%;  Pred. No. 1.6e-65;
  Matches  240;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| |||||||||||| || |||||| ||||||| ||||||||||||||||||||||||
Db        145 GGACCAGAGACGCTCTGTGGGGCTGAGTTGGTGGACGCTCTTCAGTTCGTGTGTGGAGAC 204

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||| |||||||||||||||||||| || || ||||||||||||||||||||||||||
Db        205 AGGGGTTTTTATTTCAACAAGCCCACGGGGTATGGCTCCAGCAGTCGGAGGGCACCTCAG 264

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              ||||||||||||||||||||||||||||||||||||||||||||| |||| |||||||||
Db        265 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGCGGCTAGAGATGTAC 324

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              |||||||||||||||| || ||| | |||||||| ||||||| |||||||||| ||
Db        325 TGTGCACCCCTCAAGCCTGCCAAGTCTGCCCGCTCAGTCCGTGCTCAGCGCCACACTGAC 384

Qy        241 ATGCCCAAGACTCAGAAGTA 260
              ||||||||| |||||||| |
Db        385 ATGCCCAAGGCTCAGAAGGA 404


RESULT 12
US-10-161-088-3
; Sequence 3, Application US/10161088
; Publication No. US20030077761A1
; GENERAL INFORMATION:
;  APPLICANT: Parrow, Vendela
;  APPLICANT:  Rosengren, Linda
;  TITLE OF INVENTION: NEW METHODS
;  FILE REFERENCE: 13425-111001
;  CURRENT APPLICATION NUMBER: US/10/161,088
;  CURRENT FILING DATE:  2002-05-31
;  PRIOR APPLICATION NUMBER: SE 0101934-8
;  PRIOR FILING DATE: 2001-06-01
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 286
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-161-088-3

  Query Match            40.0%;  Score 209;  DB 9;  Length 286;
  Best Local Similarity   88.3%;  Pred. No. 2.6e-59;
  Matches  227;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy         16 TGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTC 75
              ||||| |||||||||||||||||||||||||||||||||||    |||||||||| |||
Db         18 TGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCGAGGGGCTTTTACTTC 77

Qy         76 AACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCATCGTGGAT 135
              |||||||||||||| || |||||||||| |||||||||||||||||||||| ||||||
Db         78 AACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAGACAGGCATTGTGGAT 137

Qy        136 GAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCACCCCTCAAG 195
              ||||| |||||||||||||||||||||||||| |||||||||||||| || || |||
Db        138 GAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTACTGTGCCCCACTGAAG 197

Qy        196 CCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACTCAG 255
              ||  |||| |||||||||||  |||||||||||||||||||| ||||||||||||||||||

Db        198 CCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGACATGCCCAAGACTCAG 257

Qy        256 AAGTATCAGCCTCCATC 272
                  |   ||| |   ||
Db        258 GCATGCAAGCTTGTCTC 274


RESULT 13
US-09-930-377B-1
; Sequence 1, Application US/09930377B
; Patent No. US20020144296A1
; GENERAL INFORMATION:
;  APPLICANT: Wheeler, Matthew B.
;  APPLICANT:  Donovan, Sharon M.
;  APPLICANT:  Bleck, Gregory T.
;  APPLICANT:  Monaco-Seigel, Marcia
;  TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
;  FILE REFERENCE: 66-00
;  CURRENT APPLICATION NUMBER: US/09/930,377B
;  CURRENT FILING DATE:  2001-08-15
;  PRIOR APPLICATION NUMBER: 60/225,474
;  PRIOR FILING DATE: 2000-08-15
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 4532
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:alpha-LA/IGF-I
;   OTHER INFORMATION: gene construct
US-09-930-377B-1

  Query Match            35.8%;  Score 187;  DB 10;  Length 4532;
  Best Local Similarity   90.9%;  Pred. No. 2.5e-51;
  Matches  199;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       2046 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 2105

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||| |||||||||||||||||||| || || |||||||||||||||||| || |||
Db       2106 AGGGGATTTTATTTCAACAAGCCCACAGGGTATGGATCCAGCAGTCGGAGGGCGCCCCAG 2165

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       2166 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 2225

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTC 219
              || |||||||| ||||| || ||| |||| | |   ||
Db       2226 TGCGCACCCCTAAAGCCTGCCAAGTCAGCTTGATAGCTC 2264


RESULT 14
US-09-930-377B-2
; Sequence 2, Application US/09930377B
; Patent No. US20020144296A1
; GENERAL INFORMATION:
;  APPLICANT: Wheeler, Matthew B.
;  APPLICANT:  Donovan, Sharon M.
;  APPLICANT:  Bleck, Gregory T.
;  APPLICANT:  Monaco-Seigel, Marcia
;  TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
;  FILE REFERENCE: 66-00
;  CURRENT APPLICATION NUMBER: US/09/930,377B
;  CURRENT FILING DATE:  2001-08-15
;  PRIOR APPLICATION NUMBER: 60/225,474
;  PRIOR FILING DATE: 2000-08-15
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 210
```

```
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:IGF-I
US-09-930-377B-2

  Query Match             35.7%;  Score 186.6;  DB 10;  Length 210;
  Best Local Similarity   93.3%;  Pred. No. 6.4e-52;
  Matches  195;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db          1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||| |||||||||||||||||||||| || || ||||||||||||||||| || |||
Db         61 AGGGGATTTTATTTCAACAAGCCCACAGGGTATGGATCCAGCAGTCGGAGGGCGCCCCAG 120

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
              || |||||||| ||||| || ||| ||||
Db        181 TGCGCACCCCTAAAGCCTGCCAAGTCAGC 209


RESULT 15
US-10-179-046-13
; Sequence 13, Application US/10179046
; Publication No. US20030013154A1
;  GENERAL INFORMATION:
;       APPLICANT: Crawford, Kenneth
;                  Zaror, Isabel
;                  Innis, Michael
;       TITLE OF INVENTION: Pichia Secretory Leader for Protein
;                           Expression
;       NUMBER OF SEQUENCES: 40
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Chiron Corporation
;            STREET: 4560 Horton Street
;            CITY: Emeryville
;            STATE: California
;            COUNTRY: United States
;            ZIP: 94608
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/179,046
;            FILING DATE: 25-Jun-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/029,267
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Chung, Ling-Fong
;            REGISTRATION NUMBER: 36,482
;            REFERENCE/DOCKET NUMBER: 1165.100
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (510) 601-2704
;            TELEFAX: (510) 655-3542
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 390 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;            DESCRIPTION: /desc = "Synthetic"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-10-179-046-13

  Query Match             35.4%;  Score 185.2;  DB 9;  Length 390;
  Best Local Similarity   91.6%;  Pred. No. 2.6e-51;
  Matches  196;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||| |||||||||||| ||||||||||||||||||
Db        160 GGACCGGAGACGCTCTGCGGGGCTGAGCTCGTGGATGCTCTGCAGTTCGTGTGTGGAGAC 219

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||||||||||||||||||||| || |||||||||||||  |||| ||||||
Db        220 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 279

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||
Db        280 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 339

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCT 214
              || ||||||||||||| || ||| |||| | |
Db        340 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 373


Search completed: June 15, 2003, 20:22:26
Job time : 95.7296 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:41:03 ; Search time 1112.58 Seconds
(without alignments)
7613.181 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	364.8	69.8	558	9	AI503976	AI503976 vm43d08.x
c	2	363	69.4	623	10	AW146128	AW146128 um37e10.x
c	3	348.2	66.6	549	9	AI169253	AI169253 EST215088
c	4	347	66.3	558	9	AI265629	AI265629 uj04b07.x
	5	339.2	64.9	816	9	AI119218	AI119218 ue94h02.y
	6	334.8	64.0	594	12	BF383724	BF383724 602044632
c	7	322.2	61.6	499	10	AW495481	AW495481 UI-M-BH3-
c	8	320.8	61.3	642	9	AI876493	AI876493 uj59b10.x
c	9	320.8	61.3	673	14	BM984670	BM984670 UI-CF-EC1
c	10	316.8	60.6	575	9	AI248089	AI248089 qh69f05.x
c	11	309.2	59.1	468	9	AI169770	AI169770 EST215669
c	12	305	58.3	498	9	AA542914	AA542914 ni98c10.s
	13	299	57.2	882	9	AI604642	AI604642 vm43d08.y
c	14	296.4	56.7	653	14	BQ200567	BQ200567 UI-R-DZ1-
c	15	291.6	55.8	527	9	AA913900	AA913900 ol35g05.s
c	16	271.6	51.9	521	10	AW493459	AW493459 UI-M-BH3-
	17	271.6	51.9	559	13	BI715603	BI715603 ic34h10.y
	18	271.6	51.9	621	13	BI221656	BI221656 602936980
c	19	270.6	51.7	595	9	AI573421	AI573421 mo04b11.x
c	20	270	51.6	499	13	BI676839	BI676839 ic56a08.x
c	21	266.8	51.0	500	9	AA945553	AA945553 EST201052
c	22	266.8	51.0	525	9	AA963258	AA963258 UI-R-E1-g
	23	266	50.9	665	9	AA690767	AA690767 vu57d12.r
	24	265.2	50.7	559	13	BI715465	BI715465 ic33b09.y
	25	263.8	50.4	799	9	AI314558	AI314558 uj48d07.y
c	26	263.6	50.4	525	9	AI599751	AI599751 EST251454
c	27	261.4	50.0	499	13	BI294072	BI294072 UI-R-DK0-
c	28	260.4	49.8	561	13	BI714874	BI714874 ic33b09.x
c	29	258.4	49.4	502	9	AI104669	AI104669 EST213958
c	30	258	49.3	564	13	BI714981	BI714981 ic34h10.x
c	31	254.8	48.7	430	9	AI478804	AI478804 tm52e04.x
	32	254.8	48.7	558	13	BI715475	BI715475 ic33c08.y
	33	250.8	48.0	512	9	AI876203	AI876203 uj59b10.y
c	34	248.2	47.5	637	10	AW413016	AW413016 uq49h08.x
	35	246.4	47.1	473	9	AA451360	AA451360 vf84g03.r
c	36	246.4	47.1	486	9	AA993659	AA993659 ot85g11.s
	37	246.2	47.1	773	13	BI144500	BI144500 602908689
	38	243.2	46.5	482	9	AA456717	AA456717 aa13h06.r
c	39	243	46.5	474	9	AI526955	AI526955 uj48d07.x
	40	240.8	46.0	466	9	AA277619	AA277619 va80b08.r
c	41	237.6	45.4	470	9	AI233293	AI233293 EST229981
	42	237.6	45.4	608	9	AL599807	AL599807 DKFZp313O
	43	235.8	45.1	567	9	AI326648	AI326648 mo04b11.y
	44	233.2	44.6	356	10	AW297586	AW297586 UI-H-BW0-
	45	232.8	44.5	538	9	AA245300	AA245300 mx87e10.r

ALIGNMENTS

RESULT 1
AI503976/c
LOCUS AI503976 558 bp mRNA linear EST 11-MAR-1999
DEFINITION vm43d08.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1001007 3' similar to gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION AI503976
VERSION AI503976.1 GI:4401827
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 558)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

```
            MGI:565223
            This clone was previously sequenced on the 5' end only, this new
            data is from the 3' end
            High quality sequence stop: 440.
FEATURES             Location/Qualifiers
     source          1. .558
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1001007"
                     /clone_lib="Stratagene mouse diaphragm (#937303)"
                     /tissue_type="diaphragm"
                     /dev_stage="adult"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA
                     prepared from diaphragm muscle.  Primer: Oligo dT. Average
                     insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor
                     sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      103 a    133 c    149 g    173 t
ORIGIN

  Query Match           69.8%;  Score 364.8;  DB 9;  Length 558;
  Best Local Similarity  83.2%;  Pred. No. 4e-90;
  Matches  441;  Conservative    0;  Mismatches   82;  Indels    7;  Gaps    2;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||||
Db        530 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 471

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||
Db        470 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 411

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| |||||||||||||||||||||||||| ||||||||||||
Db        410 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 351

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  |||| ||||||||||| |||||||||||||||||||| |||
Db        350 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 291

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        290 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 231

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db        230 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 171

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| |  |||   | || | ||  ||||||||||| ||||||
Db        170 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 111

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||          |    |||||| | || |||  |||.      || ||||||||   ||
Db        110 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 51

Qy        475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              ||||| ||||||| ||||||||||||||||||||| ||||||||||||
Db         50 ACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATTC 1


RESULT 2
AW146128/c
LOCUS       AW146128                623 bp    mRNA    linear   EST 10-OCT-2000
DEFINITION  um37e10.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
            IMAGE:2247498 3' similar to gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AW146128
VERSION     AW146128.1  GI:6167864
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 623)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:1006958
            Seq primer: custom primer used
            High quality sequence stop: 499.
FEATURES             Location/Qualifiers
     source          1. .623
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:2247498"
                     /clone_lib="Sugano mouse embryo mewa"
                     /dev_stage="embryo, 14 dpc"
                     /lab_host="DH10B"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer  [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a  DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert.' Size selection was performed to exclude fragments
                     <1.5kb.  Library constructed by Dr. Sumio Sugano
                     (University of Tokyo Institute of Medical Science).
                     Custom primers  for sequencing: 5' end primer
                     CTTCTGCTCTAAAAGCTGCG and 3' end primer
                     CGACCTGCAGCTCGAGCACA."
BASE COUNT      123 a    138 c    170 g    191 t      1 others
ORIGIN

  Query Match           69.4%;  Score 363;  DB 10;  Length 623;
  Best Local Similarity  81.9%;  Pred. No. 1.3e-89;
  Matches  433;  Conservative    0;  Mismatches   90;  Indels    6;  Gaps    1;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || | ||| ||||||||||||||||||||||||||||||||||||||
Db        541 GGACCAGAGACCCTTTTCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 482

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||
Db        481 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 422

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| |||||||||||||||||||||||||| ||||| ||||||
Db        421 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAAATGTAC 362

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || |||||  |||| ||||||||||| |||||||||||||||||||| |||
Db        361 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 302

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        301 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 242

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
```

```
Db        241 AGAAGGAAAGGAAGTACATTTGAAGAACCCAAGTAGAGGAAGTGCAGGAAACAAGACCTA 182

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Db        181 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 122

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474

Db        121 CTGCTTGAGCAACCTGCAAAACATCGAAACCCCTACCAAATAACAATAATAAGTCCAATA 62

Qy        475 ACATTTCAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523

Db         61 ACATTACAAAGATGGGCATTTCCCCAATGAAATATACAAGTAAACATTC 13


RESULT 3
AI169253/c
LOCUS       AI169253                549 bp    mRNA    linear   EST 08-JAN-1999
DEFINITION  EST215088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
            RKIBP33 3' end, mRNA sequence.
ACCESSION   AI169253
VERSION     AI169253.1  GI:4134375
KEYWORDS    EST.
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 549)
  AUTHORS   Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
            Kerlavage,A.R. and Adams,M.D.
  TITLE     Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
            Gene Index
  JOURNAL   Unpublished (1998)
COMMENT     On Oct 6, 1998 this sequence version replaced gi:3705561.
            Other_ESTs: TC50779
            Contact: Lee, NH
            The Institute for Genomic Research
            9712, Medical Center Drive, Rockville, MD 20850, USA
            Tel: (301)-838-3529
            Fax: (301)-838-0208
            Email: nhlee@tigr.org
            Seq primer: M13-21.
FEATURES             Location/Qualifiers
     source          1. .549
                     /organism="Rattus sp."
                     /db_xref="taxon:10118"
                     /clone="RKIBP33"
                     /clone_lib="Normalized rat kidney, Bento Soares"
                     /note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
                     Site_2: NotI"
BASE COUNT      112 a    140 c    133 g    164 t
ORIGIN

  Query Match           66.6%;  Score 348.2;  DB 9;  Length 549;
  Best Local Similarity  81.8%;  Pred. No. 1.5e-85;
  Matches  428;  Conservative    0;  Mismatches   88;  Indels    7;  Gaps    2;

Qy          8 AGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCT 67

Db        549 AGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAATTCGTGTGTGGACCAAGGGGCT 490

Qy         68 TTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCA 127

Db        489 TTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGAAGGGCACCACAGACGGGCA 430

Qy        128 TCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCAC 187

Db        429 TTGTGGATGAGTGTAGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCTC 370

Qy        188 CCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCA 247

Db        369 CGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACATTGACATGCCCA 310

Qy        248 AGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGA 307

Db        309 AGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGGA 250

Qy        308 AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATG 367

Db        249 AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACTTACAGAATG 190

Qy        368 TAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCA 427

Db        189 TAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCTGCTTG 130

Qy        428 CAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATCACATTTC 481

Db        129 AGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATTTC 70

Qy        482 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523

Db         69 AGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 27


RESULT 4
AI265629/c
LOCUS       AI265629                558 bp    mRNA    linear   EST 18-NOV-1998
DEFINITION  uj04b07.x1 Sugano mouse liver mlia Mus musculus cDNA clone
            IMAGE:1890901 3' similar to gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AI265629
VERSION     AI265629.1  GI:3883787
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:975225
            Seq primer: custom primer used
            High quality sequence stop: 495.
FEATURES             Location/Qualifiers
     source          1. .558
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1890901"
                     /clone_lib="Sugano mouse liver mlia"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
                     (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                     was primed with an oligo(dT) primer
                     [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                     ligated to a  DraIII adaptor [TGTTGGCCTACTGG], digested
                     and cloned into distinct DraIII sites of the pME18S-FL3
                     vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
                     be used to isolate the cDNA insert.  Size selection was
```

performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

BASE COUNT 106 a 135 c 156 g 161 t
ORIGIN

Query Match 66.3%; Score 347; DB 9; Length 558;
Best Local Similarity 82.0%; Pred. No. 3.3e-85;
Matches 414; Conservative 0; Mismatches 85; Indels 6; Gaps 1;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||||
Db        506 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 447

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||
Db        446 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 387

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| |||||||||||||||||||||||||| ||||||||||||
Db        386 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 327

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || ||||| |||| |||||||||||  ||||||||||||||||||| |||
Db        326 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 267

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        266 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 207

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||| |||
Db        206 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 147

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| |||||||| || ||| |   ||||   | || | ||   |||||||||| ||||||
Db        146 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 87

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||          |    |||||| | || |||  |||       || |||||||   ||
Db         86 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 27

Qy        475 ACATTTCAAAGATGGCATTTCCCCC 499
              ||||| |||||||||   || ||||
Db         26 ACATTACAAAGATGGGCATTTCCCC 2
```

RESULT 5
AI119218

```
LOCUS       AI119218                816 bp    mRNA    linear   EST 02-SEP-1998
DEFINITION  ue94h02.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
            IMAGE:1498803 5' similar to gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AI119218
VERSION     AI119218.1  GI:3519542
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 816)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:936407
            Seq primer: custom primer used
            High quality sequence stop: 473.
FEATURES             Location/Qualifiers
     source          1. .816
                     /organism="Mus musculus"
                     /strain="C57BL"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1498803"
                     /clone_lib="Sugano mouse embryo mewa"
                     /dev_stage="embryo, 14 dpc"
                     /lab_host="DH10B"
                     /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
                     Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
                     with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTT];
                     double-stranded cDNA was ligated to a DraIII adaptor
                     [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
                     sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
                     CACCATGTG). XhoI should be used to isolate the cDNA
                     insert. Size selection was performed to exclude fragments
                     <1.5kb. Library constructed by Dr. Sumio Sugano
                     (University of Tokyo Institute of Medical Science).
                     Custom primers for sequencing: 5' end primer
                     CTTCTGCTCTAAAAGCTGCG and 3' end primer
                     CGACCTGCAGCTCGAGCACA."
BASE COUNT      230 a    219 c    172 g    187 t      8 others
ORIGIN
```

Query Match 64.9%; Score 339.2; DB 9; Length 816;
Best Local Similarity 81.2%; Pred. No. 5.4e-83;
Matches 389; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

```
Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| ||||||||||||||||||||||||||||||||||||||
Db        323 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 382

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||| || |||||||||| ||||||||||||||||
Db        383 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAG 442

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||| |||||||||| |||||||||||||||||||||||||| ||||||||||||
Db        443 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 502

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              ||||| || || ||||| |||| |||||||||||  ||||||||||||||||||| |||
Db        503 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 562

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db        563 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 622

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
              ||||||||||||||||||||||||||||||||||||||||| |||||| ||||||||| |||
Db        623 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCANGAAACAAGACCTA 682

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              ||| ||||| || || ||| |   ||||   | || | ||   ||||||| || ||||||
Db        683 CAGAATGTANGAGGAGCCTNCCACGGAGCAGAANATGCCACATCACCGCANGATCCTTTG 742

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAAATAAGTTTGATCACATT 479
              ||          |     ||||| | || |||  ||||| || |  | | |   || |
Db        743 CTGCTTGAGCAACCTGCANAACATCGAAACACCTACCAAATAACATNTATAAGTCCAAT 801
```

RESULT 6
BF383724

```
LOCUS       BF383724                 594 bp    mRNA    linear   EST 27-NOV-2000
DEFINITION  602044632F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4194295 5',
            mRNA sequence.
ACCESSION   BF383724
VERSION     BF383724.1  GI:11365029
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 594)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9527  row: p  column: 08
            High quality sequence stop: 589.
FEATURES             Location/Qualifiers
     source          1. .594
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4194295"
                     /clone_lib="NCI_CGAP_Li9"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.9 kb. Constructed by Life
                     Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      175 a    162 c    142 g    115 t
ORIGIN

  Query Match           64.0%;  Score 334.8;  DB 12;  Length 594;
  Best Local Similarity  82.0%;  Pred. No. 8.1e-82;
  Matches  400;  Conservative    0;  Mismatches   82;  Indels    6;  Gaps    1;

Qy         16 TGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTC 75
              ||||| ||||||||||||||||||||||||||||||||||||||   |||||||||| |||
Db        107 TGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCGAGGGGCTTTTACTTC 166

Qy         76 AACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCATCGTGGAT 135
              |||||||||||||| || |||||||||| |||||||||||||||||||||||||| ||||||
Db        167 AACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCTCAGACAGGCATTGTGGAT 226

Qy        136 GAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCACCCCTCAAG 195
              ||||| |||||||||||||||||||||||||| |||||||||||||||| || || |||
Db        227 GAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTACTGTGCCCCACTGAAG 286

Qy        196 CCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACTCAG 255
              ||  |||| |||||||||||  |||||||||||||||||||| ||||||||||||||||||
Db        287 CCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGACATGCCCAAGACTCAG 346

Qy        256 AAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGAAAGGAAGT 315
              ||||  | | | | ||| || |||||||||| ||||   || ||||||||||||||||||
Db        347 AAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGGAGAAGGAAAGGAAGT 406

Qy        316 ACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGA 375
              |||||||||||||||||||||| |||||||||||||| |||||| |||||||| ||
Db        407 ACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAATGTAGGAGGA 466

Qy        376 CCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCACAGTTACC 435
              ||| |   ||||   | || | ||   |||||||||| ||||||||           |
Db        467 GCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTGCTGCTTGAGCAACCT 526

Qy        436 TGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATCACATTTCAAAGATGG 489
                  |||||| | || ||| |||      || |||||||   || ||||| |||||||||
Db        527 GCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATAACATTACAAAGATGG 586

Qy        490 CATTTCCC 497
                 || ||
Db        587 GCATTGCC 594


RESULT 7
AW495481/c
LOCUS       AW495481                 499 bp    mRNA    linear   EST 24-FEB-2000
DEFINITION  UI-M-BH3-auy-g-11-0-UI.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
            UI-M-BH3-auy-g-11-0-UI 3', mRNA sequence..
ACCESSION   AW495481
VERSION     AW495481.1  GI:7065762
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized pineal glands library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
            clones from RESEARCH GENETICS. It should be noted that Bento Soares
            is generating a small number of additional specialized
            non-redundant arrays of BMAP cDNAs whose availability will be
            considered under appropriate and limited collaborative arrangements
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH3-auy-g-11-0-UI"
                     /clone_lib="NIH_BMAP_M_S4"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S4 library is a subtracted library of a series,
                     ultimately  derived from a mixture of individually tagged
                     normalized libraries from  ten regions of the mouse brain
                     (cerebellum, brain stems, olfactory  bulbs, hypothalamus,
                     cortex, amygdala, basal ganglia, pineal gland,  striatum,
                     hipoccampus) after a series of subtractions to reduce the
                     representation of cDNAs from which ESTs had already been
                     generated. The following serially subtracted libraries
                     were generated in this process: NIH_BMAP_M_S4,
                     NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
                     NIH_BMAP_M_S2, NIH_BMAP_M_S1.  The subtracted library
                     (NIH_BMAP_M_S4) was constructed as follows:  PCRamplified
                     cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
                     NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
                     was used as  a driver in a hybridization with a pool of
                     the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
```

libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_LIB=NIH_BMAP_M_S4
TAG_TISSUE=pineal-glands
TAG_SEQ=CAGAC"

BASE COUNT 86 a 112 c 124 g 177 t
ORIGIN

Query Match 61.6%; Score 322.2; DB 10; Length 499;
Best Local Similarity 82.3%; Pred. No. 2.3e-78;
Matches 396; Conservative 0; Mismatches 78; Indels 7; Gaps 2;

```
Qy        50 TGTGTGGAGACAGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGA 109
             ||||||||   |||||||||||| ||||||||||||||||| || |||||||||| |||||
Db       499 TGTGTGGACCGAGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGA 440

Qy       110 GGGCACCTCAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGC 169
             ||||||||||||||||||| |||||||||| |||||||||||||||||||||||||| |
Db       439 GGGCACCTCAGACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGAC 380

Qy       170 TGGAGATGTACTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGC 229
             ||||||||||||||| || || ||||| |||| ||||||||||  ||||||||||
Db       379 TGGAGATGTACTGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGC 320

Qy       230 GCCACACCGACATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGA 289
             ||||||| |||||||||||||||||||||  | | | | ||| || |||||||||| ||
Db       319 GCCACACTGACATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGA 260

Qy       290 AGTCTCAGAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGA 349
             ||   || ||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db       259 AGCTGCAAAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGA 200

Qy       350 AACAAGAACTACAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGC 409
             ||||||| |||||| |||||||| || ||| |   ||||   | || | ||   ||||||
Db       199 AACAAGACCTACAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGC 140

Qy       410 AGGACCCTTTGCTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAA 463
             |||| ||||||||           |    |||||| | || |||  |||      || ||
Db       139 AGGATCCTTTGCTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAA 80

Qy       464 TAAGTTTGATCACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATT 522
             |||||   || ||||| |||||||| ||||||||||||||||||||||||||| ||||||||||
Db        79 TAAGTCCAATAACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATT 20

Qy       523 C 523
             |
Db        19 C 19
```

RESULT 8
AI876493/c
LOCUS AI876493 642 bp mRNA linear EST 21-JUL-1999
DEFINITION uj59b10.x1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1924219 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION AI876493
VERSION AI876493.1 GI:5550542
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 642)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished (1999)
COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:980511
Seq primer: custom primer used
High quality sequence stop: 257.
FEATURES Location/Qualifiers
source 1. .642
/organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1924219"
/clone_lib="Sugano mouse liver mlia"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

BASE COUNT 127 a 154 c 175 g 185 t 1 others
ORIGIN

Query Match 61.3%; Score 320.8; DB 9; Length 642;
Best Local Similarity 80.1%; Pred. No. 6.2e-78;
Matches 403; Conservative 0; Mismatches 93; Indels 7; Gaps 2;

```
Qy         2 GACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACA 61
             |||| ||||| || ||||| |||||||||||||||||||||||| ||||||||||   |
Db       503 GACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGGTCGTGTGTGGACCGA 444

Qy        62 GGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGA 121
             |||||||||  |||||||||| ||||||| || |||||||||| | ||||||||||||||
Db       443 GGGGCTTTTTCTTCAACAAGGCCACAGGCTATGGCTCCAGCATTTGGAGGGCACCTCAGA 384

Qy       122 CAGGCATCGTGGATGAGTGCTGCTTCCGG-AGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
             ||| ||  |||||||||||| |||||||| |||||||||||||| || ||| ||||||||
Db       383 CAGTCAATGTGGATGAGTGTTGCTTCCGGAAGCTGTGATCTGAGAAGACTGNAGATGTAC 324

Qy       181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
             ||||| || || |||||  |||| ||||||||||  |||||||||||||||||||| |||
Db       323 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 264

Qy       241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
             |||||||||||||||||||  | | | | ||| || |||||||||| ||||   || |||
Db       263 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 204

Qy       301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||| |||
Db       203 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 144

Qy       361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
             ||| |||||||| || ||| |   ||||   | || | ||   |||||||||| ||||||
Db       143 CAGAATGTAGGAGGAGCCTCCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 84
```

```
Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATC 474
              ||             |     |||||| | || |||  |||      || |||||||   ||
Db         83 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 24

Qy        475 ACATTTCAAAGATGGCATTTCCC 497
              ||||| |||||||||   || ||
Db         23 ACATTACAAAGATGGGCATTTCC 1


RESULT 9
BM984670/c
LOCUS       BM984670                673 bp    mRNA    linear   EST 21-MAR-2002
DEFINITION  UI-CF-EC1-abj-k-24-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
            UI-CF-EC1-abj-k-24-0-UI 3', mRNA sequence.
ACCESSION   BM984670
VERSION     BM984670.1  GI:19610417
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 673)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: McCray, PB
            McCray Lab
            University of Iowa
            2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
            Tel: 319 356 4866
            Fax: 319 356 7171
            Email: paul-mccray@uiowa.edu
            Tissue Procurement: Dr. M. J. Welsh, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .673
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EC1-abj-k-24-0-UI"
                     /clone_lib="UI-CF-EC1"
                     /tissue_type="Lung"
                     /dev_stage="Adult and Fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-CF-EC1 is a normalized cDNA library containing the
                     following tissue(s): Normal lung from adult and from fetal
                     day 64, day 87, week 19 and week 42. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site.  Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     AAGTGCTTAC.
                     TAG_LIB=UI-CF-EC1
                     TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371
                     and 380-383
                     TAG_SEQ=AAGTGCTTAC"
BASE COUNT      152 a    164 c    169 g    188 t
ORIGIN
```

```
  Query Match           61.3%;  Score 320.8;  DB 14;  Length 673;
  Best Local Similarity   84.2%;  Pred. No. 6.2e-78;
  Matches  443;  Conservative    0;  Mismatches   27;  Indels   56;  Gaps    5;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        492 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 433

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              ||||| |||||||||| |||||||||||| || ||||||||||||||||||| ||||||
Db        432 AGGGG-TTTTATTTCAGCAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 374

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        373 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 314

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||||
Db        313 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 254

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
              |||||||||||  |||
Db        253 ATGCCCAAGACCCAG---------------------------------------------- 239

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
                     |||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        238 -------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 186

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
              |||||||||||||||||| |||||||||||||   |||| |||||||||||| ||||||
Db        185 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 126

Qy        421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
              |||||||| |||||||| ||||| |||||| |||  ||||||||||||||||| ||||
Db        125 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 66

Qy        479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
              || |||||| ||| ||||||||||||||||||||||||||||||||
Db         65 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 20


RESULT 10
AI248089/c
LOCUS       AI248089                575 bp    mRNA    linear   EST 01-DEC-1998
DEFINITION  qh69f05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:1849953 3' similar to gb:X57025_rna1 INSULIN-LIKE
            GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AI248089
VERSION     AI248089.1  GI:3843486
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 575)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 918   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 380.
FEATURES             Location/Qualifiers
     source          1. .575
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1849953"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
```

/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen 1NFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 135 a 152 c 131 g 156 t 1 others
ORIGIN

Query Match 60.6%; Score 316.8; DB 9; Length 575;
Best Local Similarity 83.8%; Pred. No. 7.6e-77;
Matches 428; Conservative 0; Mismatches 28; Indels 55; Gaps 4;

```
Qy        16 TGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTC 75
             ||||| |||||||||||| |||||||||||||||||||| |||||||||||||||||||
Db       551 TGCGGGGCTGAGCTGGTGNATGCTCTTCAGTTCGTGTGTGAAGACAGGGGCTTTTATTTC 492

Qy        76 AACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCATCGTGGAT 135
             |||||||||||||| || ||||||||||||||||||| ||||||||||||||||||||||
Db       491 AACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAGACAGGCATCGTGGAT 432

Qy       136 GAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCACCCCTCAAG 195
             |||||||||||||||||||||||||| |||||||||||||||| || ||||||||||||
Db       431 GAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAG 372

Qy       196 CCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACTCAG 255
             || || ||| |||| |||| ||||||||||||||||||||||||||||||||||||| |||
Db       371 CCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACCCAG 312

Qy       256 AAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGAAAGGAAGT 315
             ||||||||
Db       311 ----------------------------------------------------AAGGAAGT 304

Qy       316 ACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGA 375
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db       303 ACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGA 244

Qy       376 CCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTCTGCAC-AGTTAC 434
             |||| |||||||||||||  |||| |||||||||||| |||||||||||||| ||||||
Db       243 CCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTGCTCTGCACGAGTTAC 184

Qy       435 CTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTTCAAAGAT-GGCAT 492
             ||| ||||| |||||| ||| ||||||||||||||||||| |||||| |||||| ||| |
Db       183 CTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACATTTAAAAGATGGGCGT 124

Qy       493 TTCCCCCAATGAAATACACAAGTAAACATTC 523
             |||||||||||||||||||||||||||||||
Db       123 TTCCCCCAATGAAATACACAAGTAAACATTC 93
```

RESULT 11
AI169770/c
LOCUS AI169770 468 bp mRNA linear EST 20-JAN-1999
DEFINITION EST215669 Normalized rat liver, Bento Soares Rattus sp. cDNA clone RLIAT07 3' end, mRNA sequence.
ACCESSION AI169770
VERSION AI169770.1 GI:3709810
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 468)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index
JOURNAL Unpublished (1998)
COMMENT Other_ESTs: TC50779
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
FEATURES Location/Qualifiers
source 1. .468
/organism="Rattus sp."
/db_xref="ATCC (inhost):2027570"
/db_xref="taxon:10118"
/clone="RLIAT07"
/clone_lib="Normalized rat liver, Bento Soares"
/note="Organ: liver; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
BASE COUNT 85 a 115 c 119 g 149 t
ORIGIN

Query Match 59.1%; Score 309.2; DB 9; Length 468;
Best Local Similarity 81.8%; Pred. No. 9e-75;
Matches 383; Conservative 0; Mismatches 78; Indels 7; Gaps 2;

```
Qy        63 GGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGAC 122
             ||||||||| ||||||||||||||||| || |||||||||| |||||||||||| |||||
Db       468 GGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAGAC 409

Qy       123 AGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTG 182
             ||||| |||||||||||| |||| |||||||||||||||||||||| ||||||||||||
Db       408 GGGCATTGTGGATGAGTGTTGCTCCCGGAGCTGTGATCTGAGGAGGTTGGAGATGTACTG 349

Qy       183 TGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACAT 242
             ||| || || ||||| ||||| |||| || ||| |||| ||||||||||||||| ||||
Db       348 TGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACAT 289

Qy       243 GCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAG 302
             |||||||||||||||||  ||||| | ||| || |||||||||| |||| || ||||||
Db       288 GCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAG 229

Qy       303 AAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACA 362
             |||||||||||||||| |||||||||||||||||||| |||||||||||||||| |||||
Db       228 AAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACA 169

Qy       363 GGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCT 422
             | |||||||| || ||| | ||||| | || | || | | ||||||| || ||||||||
Db       168 GAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCT 109

Qy       423 CTGCACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATCAC 476
                 |    |||||| |||| ||| ||||      || ||| |||| ||  |
Db       108 GCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACC 49

Qy       477 ATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
             |||||| |||| |||||||||| ||||||||||||||||||||||||
Db        48 ATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 1
```

RESULT 12
AA542914/c
LOCUS AA542914 498 bp mRNA linear EST 19-AUG-1997
DEFINITION ni98c10.s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone IMAGE:984882 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION AA542914
VERSION AA542914.1 GI:2291394
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```
REFERENCE   1  (bases 1 to 498)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 603   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 412.
FEATURES             Location/Qualifiers
     source          1. .498
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:984882"
                     /clone_lib="NCI_CGAP_Pr21"
                     /sex="male"
                     /tissue_type="normal prostate"
                     /lab_host="DH10B"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; 1st strand cDNA was prepared
                     from normal prostate bulk tissue, and was then primed with
                     a Not I - oligo(dT) primer. Double-stranded cDNA was
                     ligated to Eco RI adaptors (Pharmacia), digested with Not
                     I and cloned into the Not I and Eco RI sites of the
                     modified pT7T3 vector.  Library is not normalized. Library
                     was constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      105 a    135 c    123 g    135 t
ORIGIN

  Query Match           58.3%;  Score 305;  DB 9;  Length 498;
  Best Local Similarity   83.5%;  Pred. No. 1.3e-73;
  Matches  440;  Conservative    0;  Mismatches   30;  Indels   57;  Gaps    6;

Qy          1 GGACCGGAGACGCTCTGCGGTGC-TGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 59
              ||||||||||   | ||||| || ||||||||||||||||||||||||||||||||||
Db        476 GGACCGGAGAACTTTTGCGGGGCTTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 417

Qy         60 CAGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCA 119
              ||||||| |||||||||||||||||||||| || ||||||||||||||||||| |||||
Db        416 CAGGGGC-TTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCA 358

Qy        120 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTA 179
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        357 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTA 298

Qy        180 CTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGA 239
              || |||||||||||||| || ||| |||| ||||| ||||||||||||||||||||||
Db        297 TTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGA 238

Qy        240 CATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAG 299
              |||||||||||| |||
Db        237 CATGCCCAAGACCCAG---------------------------------------------- 222

Qy        300 GAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACT 359
                  |||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        221 --------AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACT 170

Qy        360 ACAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTT 419
              |||||||||||||||||| |||||||||||||  |||| ||||||||||| |||||
Db        169 ACAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTT 110

Qy        420 GCTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACA 477
              |||||||| |||||||| ||||| |||||| ||  |||||||||||||||| |||
Db        109 GCTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACA 50

Qy        478 TTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
                  ||| |||||| ||| ||||||||||||||||||||||||||||||||
Db         49 TTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 3


RESULT 13
AI604642
LOCUS       AI604642                882 bp    mRNA    linear   EST 21-APR-1999
DEFINITION  vm43d08.y1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA
            clone IMAGE:1001007 5' similar to gb:M11568 INSULIN-LIKE GROWTH
            FACTOR IB PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for
            preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
ACCESSION   AI604642
VERSION     AI604642.1  GI:4613809
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 882)
  AUTHORS   Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
            Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
            ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
            ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
            Waterston,R. and Wilson,R.
  TITLE     The WashU-NCI Mouse EST Project 1999
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Marra M/WashU-NCI Mouse EST Project 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:565223
            This read is a RESEQUENCE of a previously sequenced mouse clone
            This read has been verified (found to hit its original self in the
            correct orientation)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 361.
FEATURES             Location/Qualifiers
     source          1. .882
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1001007"
                     /clone_lib="Stratagene mouse diaphragm (#937303)"
                     /tissue_type="diaphragm"
                     /dev_stage="adult"
                     /lab_host="SOLR (kanamycin resistant)"
                     /note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
                     EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA
                     prepared from diaphragm muscle.  Primer: Oligo dT. Average
                     insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor
                     sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'
                     CTCGAGTTTTTTTTTTTTTTTT 3'"
BASE COUNT      236 a    226 c    183 g    223 t     14 others
ORIGIN

  Query Match           57.2%;  Score 299;  DB 9;  Length 882;
  Best Local Similarity   77.2%;  Pred. No. 7.3e-72;
  Matches  393;  Conservative    0;  Mismatches  109;  Indels    7;  Gaps    3;

Qy          1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
              ||||| ||||| || ||||| |||||||||| ||||||||||||||||||||||||||
Db        377 GGACCAGAGACCCTTTGCGGNGCTGAGCTGNTGGATGCTCTTCAGTTCGTGTGTGGACCG 436

Qy         61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
              |||||||||||| |||||||||||||||||| || |||||||||| |  ||||||||||||
Db        437 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTTCGAGGGCACCTCAG 496

Qy        121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
```

```
Db        497 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGANGAGACTGGAGATGTAC 556

Qy        181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Db        557 TGTGCCCCACTGAAGCCTACANAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 616

Qy        241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Db        617 ATGCNNCAGACTCAGAAGTCCCCGTNCCTATCGACNNAACAGAAAACGAAGCTTGCAAGG 676

Qy        301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Db        677 GAGAGGGAAGGGAGTACATTTGAGGAACACANGTNGAGGAAGTGCANGAAACAAGACCTA 736

Qy        361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Db        737 CCAGATGTANGAGGAGCCTTC--AACCGAGCAGAAATGCACATCACCCGNAGATCCTTTG 794

Qy        421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAA----AAAATAAGTTTGATCAC 476

Db        795 CT-GCTTGAGCTAACTGCAAACATCGAACCACTTACCAATTACAATAATAAGTTCAATAA 853

Qy        477 ATTTCAAAGATGGCATTTCCCCCAATGAA 505

Db        854 CATACAAAGATGGCATTTCCCCCATTGAA 882


RESULT 14
BQ200567/c
LOCUS       BQ200567                653 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  UI-R-DZ1-cne-a-18-0-UI.s1 UI-R-DZ1 Rattus norvegicus cDNA clone
            UI-R-DZ1-cne-a-18-0-UI 3', mRNA sequence.
ACCESSION   BQ200567
VERSION     BQ200567.1  GI:20417032
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 653)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to verify it as a clone from the
            normalized cartilaginous tumor library cDNA Library Preparation:
            M.B. Soares Lab Clone distribution: clones will be available
            through Research Genetics (www.resgen.com) The following repetitive
            elements were found in this cDNA sequence: 1-43,
            >AT_rich#Low_complexity 118-164, >POLY_A#Simple_repeat
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .653
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-DZ1-cne-a-18-0-UI"
                     /clone_lib="UI-R-DZ1"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="37 days"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Organ: Spine; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     UI-R-DZ1 is a normalized cDNA library containing the
                     following tissue(s): Swarm Rat Chondrosarcoma. The library
                     was constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     CATTCTTGTA. The Rat cartilaginous tumor tissue was
                     provided by Dr Jeff Stevens at the University of Iowa.
                     TAG_LIB=UI-R-DZ1
                     TAG_TISSUE=cartilaginous tumor
                     TAG_SEQ=CATTCTTGTA"
BASE COUNT      134 a    137 c    137 g    245 t
ORIGIN

  Query Match           56.7%;  Score 296.4;  DB 14;  Length 653;
  Best Local Similarity  81.9%;  Pred. No. 3.5e-71;
  Matches  380;  Conservative    0;  Mismatches   76;  Indels    8;  Gaps    3;

Qy         67 TTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGC 126

Db        653 TTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGCACCACAGACGGGC 594

Qy        127 ATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCA 186

Db        593 ATTGTGGATGAGTG-TGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCT 535

Qy        187 CCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCC 246

Db        534 CCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGACATGCCC 475

Qy        247 AAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGG 306

Db        474 AAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGG 415

Qy        307 AAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGAT 366

Db        414 AAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAAT 355

Qy        367 GTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGC 426

Db        354 GTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGTTGCTT 295

Qy        427 ACAGTTACCTGTAAACATTGGAATACCGGCCA------AAAAATAAGTTTGATCACATTT 480

Db        294 GAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATTT 235

Qy        481 CAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523

Db        234 CAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTC 191


RESULT 15
AA913900/c
LOCUS       AA913900                527 bp    mRNA    linear   EST 24-SEP-1998
DEFINITION  ol35g05.s2 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1525496 3' similar to gb:X57025_rna1 INSULIN-LIKE GROWTH
            FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AA913900
VERSION     AA913900.1  GI:3053292
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 527)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 870   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 97.
FEATURES             Location/Qualifiers
     source          1. .527
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1525496"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
BASE COUNT      125 a    134 c    119 g    149 t
ORIGIN

  Query Match           55.8%;  Score 291.6;  DB 9;  Length 527;
  Best Local Similarity   82.8%;  Pred. No. 6.9e-70;
  Matches  404;  Conservative    0;  Mismatches   29;  Indels   55;  Gaps    4;

Qy         39 TCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTC 98
              ||||||||||||||||||||||||||||||||  || ||||||||||||||| || |||||
Db        527 TCTTCAGTTCGTGTGTGGAGACAGGGGCTTTATTTACAACAAGCCCACAGGGTATGGCTC 468

Qy         99 CAGCAGTCGGAGGGCACCTCAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGA 158
              ||||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||
Db        467 CAGCAGTCGGAGGGCGCCTAAGACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGA 408

Qy        159 TCTGAGGAGGCTGGAGATGTACTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGT 218
              ||| ||||||||||||||||| || |||||||||||||| || ||| |||| ||||| ||
Db        407 TCTAAGGAGGCTGGAGATGTATTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGT 348

Qy        219 CCGTGCCCAGCGCCACACCGACATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAA 278
              |||||||||||||||||||||||||||||||| |||
Db        347 CCGTGCCCAGCGCCACACCGACATGCCCAAGACCCAG---------------------- 311

Qy        279 CAAGAAAATGAAGTCTCAGAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAG 338
                                              |||||||||||||||||| |||||||||
Db        310 ----------------------------AAGGAAGTACATTTGAAGAACGCAAGTAGAG 280

Qy        339 GGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGA 398
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||  ||
Db        279 GGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGA 220

Qy        399 CAGGCCACCGCAGGACCCTTTGCTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGC 456
              || |||||||||||| |||||||||||||| ||||||||| ||||| |||||| |||  |
Db        219 CATGCCACCGCAGGATCCTTTGCTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTAC 160

Qy        457 CAAAAAATAAGTTTGATCACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGT 515
              |||||||||||||||| |||||| |||||| ||| ||||||||||||||||||||||||
Db        159 CAAAAAATAAGTTTGATAACATTTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGT 100

Qy        516 AAACATTC 523
              ||||||||
```

```
Db         99 AAACATTC 92


Search completed: June 15, 2003, 18:18:25
Job time : 1114.58 secs
```